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1			222.0,0		818-1073
					1163-3038
HBJDZ49	9502	847928	AC004980	42383	1-293
HBJDZ49	9502	847928	AC004980	42384	1-1417
	1202	1017720	110004900	172304	1-141/

HBJDZ49	9502	847928	AC005073	42385	1-513
	7502	017320	AC005075	42363	2138-2341
					2878-3828
				-	4039-4407
4					4438-5711
1					6598-6908
					6969-7501
					7547-7645
					7882-8496
					8569-9146
					9288-11595
					11642-11927
					12146-12299
					12591-12757
					13029-13369
					13719-14460
					14563-14623
					14696-15271
					15352-16582
					16831-17249
					17276-17914
					17947-18016
					18327-19493
		ļ			19719-20635
		į			21271-22015
			ľ		22432-22985
					23034-23359
				1	24795-25234
					26499-26923
				ŀ	27475-28264
					28742-29110
					29565-29655
					29657-29867
					30539-30779
					31272-31718
HBJDZ49	9502	847928	AC005073	42386	1-257
HBJDZ49	9502	847928	AC018720	42387	1-1380
HBJDZ49	9502	847928	AC006480	42388	1-1207
HBJDZ49	9502	847928	AC006480	42389	1-327
HBJDZ49	9502	847928	AF030453	42390	1-583
HBJDZ49	9502	847928	AF030453	42391	1-3119
		ŀ			3130-4112
HBJDZ49	9502	847928	AC004867	42392	1-868
					1145-2855
					2954-4494
					4586-5798
					5910-9476
					10040-10848
					11092-11171
					11330-11695
					12154-12509
					13065-13372
					13935-14448
HBJDZ49	9502	847928	AC004867	42393	1-583
	7502	04/920	AC004607	42393	
HBJDZ49	9502	847928	AC005088	42394	834-1954
HBJDZ49	9502	847928			1-583
LIJUULAN	3302	04/920	AC005088	42395	1-3121

IID ID Z 40					3128-4110
HBJDZ49	9502	847928	AC005488	42396	1-867
					1144-2852
					2949-4487
					4579-5789
					5978-9485
					10048-10911
					11334-11700
					12034-12509
					13205-13321
					13907-14417
HBJDZ49	9502	847928	AC005488	42397	1-735
					738-975
HBJDZ49	9502	847928	AC005098	42398	1-866
		*			1143-2850
J	J]		J	2949-4489
					4581-5793
		Ì			5905-8184
					8255-9460
			`		10026-10834
					11078-11157
					11307-11672
		į			12131-12486
					13183-13299
					13912-14426
HBJDZ49	9502	847928	AC005098	42399	1-937
HBJDZ49	9502	847928	AC004166	42400	1-868
		101725	110001100	72700	1146-2858
					2957-4497
					4589-5801
					5913-9479
				1	10043-10851
					11095-11174
		,			11333-11698
					12157-12512
HBJDZ49	9502	847928	AC004166	42401	13938-14451
	3302	047720	AC004100	42401	1-583
HBJDZ49	9502	847928	AC005071	12102	834-1954
HBJDZ49	9502	847928		42402	1-896
111030279	3302	04/920	AC061712	42403	1-1123
					1396-3493
	ł			}	3581-3836
					3838-7040
UD ID 740	0502	0.47000	1.0005051		7048-8923
HBJDZ49	9502	847928	AC005071	42404	1-513
					2138-2341
	İ				2878-3828
					4039-4407
					4438-5711
					6609-6900
					6969-7501
					7547-7645
					7882-8496
		.			8569-9146
	}				9288-11595
					11642-11927
					12146-12299

1					12591-12757
					13029-13369
İ	ŀ				13719-14460
					14563-14623
					14709-15271
					15352-16582
					16831-17249
					17276-17914
					17947-18016
					18327-19493
					19719-20635
					21586-21816
					24795-25126
1					26501-26923
				1	27475-28264
					28742-29110
					29565-29655
					29657-29867
HBJDR24	9503	677407	4.0000051	40.40.5	31272-31718
HBJDR24	9503	677407	AC009951	42405	1-642
HBJDR24	9503	677407	AC009951	42406	1-327
IIDJDK24	9303	677407	AC009951	42407	1-486
HBJDQ86	9504	704654	17.100.710		993-1122
UDIDO90	9304	784654	AL133548	42408	1-50
					3009-3073
					4198-4253
					5692-5831
					6776-6827
					8851-8970
					9968-10050
					12598-12974
					13262-13364
					16417-16776
HBJDQ86	9504	784654	AT 122540	12.100	19112-20566
HBJDM70	9505		AL133548	42409	1-1017
		757435	AC010894	42410	1-380
HBJDM70	9505	757435	AC010894	42411	1-502
HBJDL24	9506	678272	AC008675	42412	1-996
HBJDL24	9506	678272	AC008675	42413	1-300
HBJCQ65	9508	876430	AF192303	42414	1-1230
IIDIGIOO	0500				1271-3810
HBJCJ82	9509	779645	AL161456	42415	1-1118
HBJCJ82	9509	779645	AL158075	42416	1-1523
HBJCJ82	9509	779645	AL158075	42417	1-853
77777070					1340-2553
HBJCJ82	9509	779645	AL158075	42418	1-482
HBJCE07	9510	954090	AC025605	42419	1-357
					443-919
HBJCE07	9510	954090	AC073101	42420	1-357
HBJCE07	9510	954090	AC025605	42421	1-653
HBJCE07	9510	954090	AC073101	42422	1-233
HBJCE07	9510	954090	AC073101	42423	1-420
HBJBR04	9512	847952	AC005682	42424	1-458
HBJBR04	9512	847952	AC005682	42425	1-373
HBJAP95	9513	796659	AL138715	42426	1-1044
HBJAP95	9513	796659	AL031601	42427	1-590
					1338-1600
					1556-1000

					2644-3247
HBJAP95	9513	796659	AL138715	42428	1-717
HBJAP95	9513	796659	AL138715	42429	1-265
HBJAP95	9513	796659	AL031601	42430	1-706
HBJAJ49	9515	723164	AC078846	42431	1-416
					1103-1882
HBJAJ49	9515	723164	AC078846	42432	1-116
HBJAH27	9517	682941	AC016325	42433	1-69
					560-632
					2298-2395
					2510-2613
	}	İ			3563-3801
					5031-5598
HBJAE32	9518	600605	A C044042	10.40.4	5763-5801
IIDJAE52	9318	699695	AC044843	42434	1-487
HBJAE32	9518	600605	A C000525	10.12.5	983-1447
IIDJAE52	9318	699695	AC008525	42435	1-487
HBJAE32	9518	699695	A C000525	42426	983-1447
HBJAB49	9520	722195	AC008525	42436	1-337
HBJAB49	9520	722195	AF276759	42437	1-1613
HBJAB49	9520	722195	AC019031	42438	1-1613
HBJAB49	9520	722195	AF276759	42439	1-561
HBJAB28	9521	847966	AC019031	42440	1-561
HBJAB15	9522	660552	AC023071	42441	1-736
HBJAB15	9522	660552	AP001931	42442	1-1266
HBJAB15	9522	660552	AP000727	42443	1-1264
HBJAB15	9522		AP001931	42444	1-366
HBJAB15	9522	660552	AP001931	42445	1-308
HBJAB15	9522	660552	AP000727	42446	1-366
HBDAE47	9523	720008	AP000727	42447	1-308
HBDAE47	9523	720008	AL353776	42448	1-1591
HBDAD16	9525	661560	AL353776	42449	1-490
HBDAD16	9525		AC013396	42450	1-1371
HBDAD16	9525	661560 661560	AC013396	42451	1-296
HBCCO10	9526	963157	AC013396	42452	1-204
HBCCO10	9526		AC009634	42453	1-575
HBCCO10	9526	963157	AC011721	42454	1-575
HBCCO10	9526	963157	AC009634	42455	1-206
HBCCO10	9526	963157 963157	AC011721	42456	1-206
HBCCJ05	9527		AC011721	42457	1-86
HBCCJ05	9527	930956	AC068322	42458	1-600
HBCCJ05	9527	930956	AC027243	42459	1-600
HBCCJ05	9527	930956	AC024059	42460	1-600
HBCCJ05	9527	930956	AC010868	42461	1-584
HBCCJ05	9527	930956	AC068322	42462	1-424
HBCCJ05	9527	930956 930956	AC027243	42463	1-456
IIDCCiO	9327	930936	AC068322	42464	1-460
HBCCJ05	9527	020056	A C027242	42465	1112-1585
COLOCULA	3341	930956	AC027243	42465	1-460
HBCCJ05	9527	930956	A C024050	12166	1112-1585
HBCCJ05	9527	930956	AC024059	42466	1-456
HBCCJ05	9527	930956	AC010868	42467	1-385
HBCCD06			AC010868	42468	1-335
1100000	9529	938319	AC007783	42469	1-2334
					2508-3084
			_ <u>, </u>		3578-3890

					
1					4198-4294
					4376-4623
					4712-5349
					5369-6088
					6527-7107
					7298-7392
			Í		7730-7846
					9147-9476
					10487-10575
				į	10791-11298 11485-11601
					11783-13009
					13207-13501
					13540-13772
					14439-14800
					14923-14983
					15133-15355
					15485-15653
					16750-16805
					16894-17078
					17162-17219
		1			18003-18089
					21085-21146
					21358-21501
HBCCD06	9529	938319	AC007783	42470	1-308
HBCCD06	9529	938319	AC007783	42471	1-1024
HBCCB51	9530	975256	AL139353	42472	1-71
					265-794
					1791-2077
IID CDNIs1	0522	0.500.55			2409-2656
HBCBN51	9532	952057	AC073846	42473	1-141
			ļ		323-951
					1073-1625
HBCBN51	9532	952057	AC073846	42474	1640-2371
HBCBF12	9535	969578	AC068735	42474	1-285
HBCBF12	9535	969578	AC008733 AC021725	42476	1-530
HBCBF12	9535	969578	AL021723 AL021368	42477	1-534 1-382
IIDODI IZ	7555	909378	AL021308	424//	762-1102
					1231-1761
HBCBF12	9535	969578	AC068735	42478	1-342
HBCBF12	9535	969578	AC021725	42479	1-342
HBCBF12	9535	969578	AC068735	42480	1-659
HBCBF12	9535	969578	AC021725	42481	1-679
HBCBF12	9535	969578	AL021368	42482	1-664
HBCBF12	9535	969578	AL021368	42483	1-307
HBCBE57	9536	848322	AL031666	42484	1-1235
HBCBE57	9536	848322	AL031666	42485	1-508
HBCBE57	9536	848322	AL031666	42486	1-648
HBCBB22	9537	848325	AC010735	42487	1-900
HBCAT10	9539	968195	AL357521	42488	1-374
HBCAT10	9539	968195	AL021528	42489	1-374
HBCAT10	9539	968195	AL357521	42490	1-689
HBCAT10	9539	968195	AL357521	42491	1-355
HBCAT10	9539	968195	AL021528	42492	1-689
HBCAT10	9539	968195	AL021528 AL021528	42493	1-355
	12222	700193	ALV21340	142473	1-333

HBCAS32	9540	699489	AC007101	42494	1-215
				1.2.2	867-1214
					1226-2260
					2359-2415
HBCAQ85	9541	783431	AC019071	42495 .	1-831
ļ			}		1116-1365
					1600-1920
ľ	1				2161-2334
					2902-3156
					3364-3836
					4074-4278
					4306-4417
					4485-4581
					4693-4853
				1	4995-5264
					5758-5863
					6411-6509
IIDCA 005	0541				6551-6922
HBCAQ85	9541	783431	AC019071	42496	1-412
HASCG58	9543	738423	AC011116	42497	1-869
HASCG58	9543	738423	AC078794	42498	1-870
HASCG58	9543	738423	AC011116	42499	1-971
HASCG58	9543	738423	AC078794	42500	1-623
HASCG58	9543	738423	AC011116	42501	1-623
HASAW90	9544	789112	AC010234	42502	1-2931
HASAW90	9544	789112	AC021464	42503	1-58
					332-547
					909-1209
					2280-2634
					3445-3539
					4477-4620
					7577-10496
					12087-13447
	l				13462-15091
TTAGATTEG					15142-16137
HASAW90	9544	789112	AC021464	42504	1-506
HASAC10	9546	968746	AC007677	42505	1-477
HASAC10	9546	968746	AC007677	42506	1-1410

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID	Contig	SEO	Analysis	PFam/NR Description	PFam/ND Assession	Comme	ATT	
Z:ON	ë	NO:X	Method		Number	Percent	From	NI 10
HAMHB21	961376	11	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	100	497	916
HBDAC79	935414	26	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
			blastx.14	(AL021958) fadE9	gi 2911026 emb CAA	62%	94	255
			,	Mycobacterium	17519.1	51%	. 250	384
			····	tuberculosis		64%	348	422
HBJAG72	722723	32	HMMFR	DFAM: Zing binding	DECOCOO	3370	0	68
		1	1.8	metalloprotease domain	rruuuyy	7.37	83	115
HBJGT92	919507	107	HMMER 1.8	PFAM: Bacterial mutT	PF00293	7.68	377	436
HBJIY20	669519	141	HMMER 2.1.1	PFAM: Orn/Lys/Arg	PF01276	53.1	49	162
.HBMBU24	677240	234	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.72	139	192
HBMBZ71	880580	238	HMMER 1.8	PFAM: von Willebrand factor type D domain	PF00094	26.52	200	526
HBMDC16	888206	258	blastx.2	Butyrophilin-like protein BUTR-1.	sp AAF72554 AAF72 554	20%	19	315
HBMU090	928078	294	blastx.14	Zfp61p [Mus musculus]	gi 887887 gb AAC52	84%	24	119
HBMXE31	573323	317	HMMER 1.8	PFAM: Gonadotropin- releasing hormones	PF00446	10.78	112	141
HCFCF47	894415	372	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	89.54	20	295
HCFCJ21	671028	374	HMMER	PFAM: Core histones	PF00125	12.79	123	188

			1.8	H2A H2B H3 and H4				
HCFLE95	945122	391	blastx.14	p34 protein [Rattus sp.]	gi[534876 dhi[BAA02	81%	176	101
					8455 107 9 4 5 J 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	100%	726	191
					1	85%	250	2/1
HCUAL07	953876	449	blastx.14	(AF079098) arginine- tRNA-protein transferase	gi 3806094 gb AAD1	87%	5	97
				1-1p; ATE1-1p [Homo				
HCUBJ11	967484	478	blastx.14	Ps 2=basic proline-rich	gi 386433 gb AAB27	37%	158	63
				protein(PRB1L precursor	289.1	53%	62	24
	•			1 1 [Homo sapiens]		35%	325	242
				,		40%	133	59
						78%	158	63
			···	-		40%	133	59
			***			36%	225	160
						36%	225	160
						41%	74	24
						41%	74	24
						32%	325	242
						33%	158	87
						36%	158	93
						36%	183	118
						71%	44	24
						71%	44	24
TUTINTER	015740	072	un o ur			35%	74	24
ncoD163	913/42	248	HMMER 2.1.1	PFAM: tRNA synthetases class II (A)	PF01411	35.1	269	930
			blastx.14	ORF YNL040w	gi 1301892 emb CAA	42%	763	972
				[Saccharomyces	95907.1	52%	859	759
				cerevisiae		31%	1153	1293
						42%	1678	1740

1149	1494	42	226	284	-)	73	387	5	83	32	301	275	51	179	222	257	166	65	8	291	266	306
1009	1273	13	173	102	1	2	316	7.00	C57	70	321	45	13	6	202	228	65	6	316	344	153	262
21%	20%	5.43	7.99	73.02		4.81	3.55	7027	47.70	46%	71%	78.2	9.77	63%	85%	%09	85%	84%	%65	55%	79%	46%
		PF00196	PF00020	PF00106		PF00505	PF00018	mil16537771db;IB A A 1	6107 1 2010 1 2010 1 2010 1 2010	818/.1		PF01514	PF00010	gi 42759 emb CAA25	537.1		gi 1655655 emb CAB	03723.1	gi 43952 emb CAA43	389.1	gi 309183 gb AAA37	443.1
	4 4 4 1	Pr AM: Bacterial regulatory proteins, luxR family	PFAM: TNFR/NGFR cysteine-rich region	PFAM: Alcohol/other	dehydrogenases, short chain type	PFAM: HMG (high	PFAM: Src homology	hynothetical protein	Campohogantia and	[Synechocysus sp.]		PFAM: Secretory protein of YscJ/FiiF family	PFAM: Helix-loop-helix DNA-binding domain	URF (pot. 4.5S protein)	[Escherichia coli]		lepA [Mycobacterium	tuberculosis	xylose isomerase	K lebsiella pneumoniae	collagen type XVII [Mus	musculus
	4.00	HMMEK 1.8	HMMER 1.8	HMMER	1.8	HMMER	HMMER 1.8	blastx.14				HMMER 2.1.1	HMMER 1.8	blastx.14			blastx.14		blastx.14		blastx.14	
	202	393	647	029		702	748	759				782	799	608			810		812	100	825	
	054057	70407	880730	706471		615198	702435	932623				66/283	968515	967717		0000	934909		921653	007700	924638	
	HCITEI110		HCUGB48	HCUGR38		HCUHM44	HCWAK80	HCWAR05			Troum of	HCWBB63	HCWBE76	HCWBI37		TOTTOTTO	HC WBIS3	110110100	HCWBI90	TICHTONIO	HC WBINU6	

			259 303	310 357			147 287			31 264	220 381		117 167			25 198			121 168		15 179	9 215	18 200			416 613		100
,000	0//0	36%	46%	43%	75%	42%	42%	54%		69.62	80	<u> </u>	82%	87%	*****	27.3			4.63		62.98	%69	44%	51%	41%	81.59		%62
			-				gi 536588 emb CAA8	5172.1		PF00501	PF01991		gi 2506078 dbj BAA2	2622.1		PF00497			PF00099		PF00005	gb AAC76377.1				PF00196		gil151190 gh AAA25
							ORF YBR208c	[Saccharomyces	Privile Andre 1: 1:	FFAM: AMP-binding enzymes	PFAM: ATP synthase	(E/31 kDa) subunit	tetracycline transporter-	like protein [Mus	musculus]	PFAM: Bacterial	extracellular solute-	binding proteins, family 3	PFAM: Zinc-binding	metalloprotease domain	PFAM: ABC transporters	(AE000411) putative	ATP-binding component	of a transport system	[Escherichia coli]	PFAM: Bacterial	regulatory proteins, luxR family	copC peptide
	122						blastx.14		Th A AT	HIMIMEK 1.8	HMMER	2.1.1	blastx.14			HMMER	2.1.1		HMMER	1.8	HMMER 1.8	blastx.2				HMMER		blastx.14
							834		100	091	606		945			952			957		973					993		1014
_	·					,	988076		520220	727230	693632		924632			527555			889416		839104					974478		967361
						S C C C C C C C C C C C C C C C C C C C	HCWBQ03		HCWCMES		HCWCR31		HCWDI64			HCWDJ23			HCWDL45		HCWDR01					HCWDV17		HCWDX22

gil4378174 gb AAD1 50% 44 58% 9 9 55% 38 gil56463 emb CAA68 75% 481 759.1 PF00099 2.79 57 gil557259 emb CAA5 55% 360 7572.1 gil887431 emb CAA5 75% 300 2057.1 gil887431 emb CAA5 75% 300 gil887431 emb CAA5 75% 300 gil2635409 emb CAB 54% 365 14904.1 gil2443870 gb AAB8 100% 37 1 1544.1 66% 5 PF00183 10.32 37 1 gil3724045 emb CAA 325% 32% 3					[Pseudomonas syringae]	808.11	81%	173	250
Expansion Expa	HCWDX76	932614	1019	blastx.14	(AF102543) unknown	gil4378174 gh AAD1	20%		220
971865 1041 blastx.14 gp210 (AA 1-1886) gi 55463 emb CAA68 75% 38					[Zymomonas mobilis]	9419.1	%85	6	50
971865 1041 blastx.14 gp210 (AA 1-1886) gij56463 emb CAA68 75% 481 948693 1058 HMMER PFAM: Zinc-binding PF00099 2.79 57 948693 1058 HMMER PFAM: Zinc-binding PF00099 8.6 226 948690 1066 HMMER PFAM: Zinc-binding PF00099 8.6 226 1.8 metalloprotease domain gil887431 emb CAA5 75% 300 1.8 metalloprotease domain gil887431 emb CAA5 75% 30 1.8 metalloprotease domain gil887431 emb CAA5 75% 30 1.8 metalloprotease domain gil887431 emb CAA5 75% 30 1.8 metalloprotease domain gil887431 emb CAA5 75% 30 1.8 metalloprotease domain gil887431 emb CAA5 75% 30 2.057.11 dehydrogeanse gil3128267 gb AAC1 39% 34 3.069 blastx.14 (AF010496) exonuclease gil3C35409 emb CAB 77% 19						-	55%	38	49
Frantius norvegrous 1799.1 Frantius norvegrous 1058 HMMER PFAM: Zinc-binding PF00099 2.79 57 18 Englishoriease domain Pf00099 87% 248	HCWED61	971865	1041	blastx.14	gp210 (AA 1-1886)	gi 56463 emb CAA68	75%	481	212
P48693 1058					Kattus norvegicus	759.1			
1.8 metalloprotease domain 1.8 metalloprotease domain 1.8 metalloprotease domain 1.8 metalloprotease domain 1.8 metalloprotease domain 1.8 metalloprotease domain 1.8 metalloprotease domain 2057.1 2057.1	HCWEG69	948693	1058	HMMER	PFAM: Zinc-binding	PF00099	2.79	57	86
948690 1066 HMMER PFAM: Zinc-binding PF00099 8.6 248 56 5772.1 8772.1 8776 56 56 56 56 56 56 56			~~~~	1.8	metalloprotease domain				
948690 1066 HMMER PFAM: Zinc-binding PF00099 8.6 226 1.8 metalloprotease domain gil887431 emb CAA5 75% 300 916972 1086 blastx.14 formaldehyde gil887431 emb CAA5 75% 300 916972 1086 blastx.14 (AF010496) exonuclease gil3128267 gb AAC1 39% 34 920887 1096 blastx.14 (AF010496) exonuclease gil2635409 emb CAB 57 908245 1105 HMMER PFAM: DEAD and PF00270 72.08 37 18 DEAH box helicases gil2443870 gb AAB8 100% 37 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 103.2 37 954142 1125 blastx.14 (AJ000758) precorrin-4 gil3724045 emb CAA 32% 3 megalerium] megalerium 04314.1 04314.1 32% 3				blastx.14	orf3 [Pseudomonas	gi 557259 emb CAA5	55%	248	45
948690 1066 HMMER PFAM: Zinc-binding PF00099 8.6 226 1.8	0110111011	0000	,		aeruginosa	7572.1	87%	99	6
1.8 metalloprotease domain blastx.14 formaldehyde 2057.1 (glutathione) [Escherichia coli] 2057.1 (afvolutathione) [Escherichia coli] 2057.1 (AF010496) exonuclease 2057.1 47% 193 200887 1086 blastx.14 (AF010496) exonuclease 2019.1 47% 193 200887 1096 blastx.14 argininosuccinate lyase 2019.1 47% 2019.1 47% 2019.20887 1096 blastx.14 (AF010496) exonuclease 2019.20887 2019.2	HCWEII9	948690	1066	HMMER	PFAM: Zinc-binding	PF00099	9.8	226	273
Plastx.14 formaldehyde Gi 887431 emb CAA5 75% 300				1.8	metalloprotease domain				
Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) [Escherichia coli] Glutathione) Glutat				blastx.14	formaldehyde	gi 887431 emb CAA5	75%	300	10
106972 1086 blastx.14 (AF010496) exonuclease gij3128267 gb AAC1 39% 34 1 200887 1096 blastx.14 argininosuccinate lyase gi2635409 emb CAB 54% 365 908245 1105 HMMER PFAM: DEAD and PF00270 72.08 37 1 1.8 DEAH box helicases blastx.14 (AC002985) R27090_2 gi]2443870 gb AAB8 100% 37 1 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 954142 1125 blastx.14 (AJ000758) precorrin-4 gij3724045 emb CAA 32% 3 22 methylase [Bacillus 04314.1 methylase [Bacillus 1041.1 methylase [Bacillus					dehydrogenase	2057.1		•) (
916972 1086 blastx.14 (AF010496) exonuclease gi[3128267]gb AAC1 39% 34 1 920887 1096 blastx.14 argininosuccinate lyase gi[2635409]emb CAB 54% 365 1 908245 1105 HMMER PFAM: DEAD and PF00270 PF00270 72.08 37 1 1 908245 1105 HMMER PFAM: DEAD and PF00270 PF00270 72.08 37 1 1 1.8 DEAH box helicases gi[2443870]gb AAB8 100% 37 1 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 954142 1125 blastx.14 (AJ000758) precorrin-4 gi[3724045]emb CAA 32% 3 2 methylase [Bacillus methylase [Bacillus 04314.1 32% 3 2	.,				(glutathione) [Escherichia	-			
916972 1086 blastx.14 (AF010496) exonuclease gi[3128267]gb AAC1 39% 34 1 920887 1096 blastx.14 argininosuccinate lyase gi[2635409]emb CAB 54% 365 1 908245 1105 HMMER PFAM: DEAD and PF00270 PF00270 72.08 37 1 1 908245 1105 HMMER PFAM: DEAD and PF00270 PF00270 72.08 37 1 1 Bacillus subtilis] 14904.1 A7% 57 1 1 Bacillus subtilis] 14904.1 A7% 37 1 1 Bacillus subtilis] 15443870 gb AAB8 100% 37 1 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 954142 1125 blastx.14 (AJ000758) precorrin-4 gi[3724045 emb CAA 32% 3 2 methylase [Bacillus 04314.1 A7% 32% 3 2					colij				
SbCD homolog ShCD homolog G119.1 47% 193 2 P20887 1096 blastx.14 argininosuccinate lyase gi[2635409 emb CAB 54% 365 37 1 P08245 1105 HMMER PFAM: DEAD and PF00270 72.08 37 1 P108245 1105 HMMER PFAM: DEAD and PF00270 72.08 37 1 P108245 1105 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 P571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 P54142 1125 blastx.14 (AJ000758) precorrin-4 gi[3724045 emb CAA 32% 3 2.2 methylase [Bacillus 04314.1 methylase [Bacillus methylase [Bacillus 04314.1 methylase [PFAM: Heathy	HCWEL01	916972	1086	blastx.14	(AF010496) exonuclease	gi 3128267 gb AAC1	39%	34	171
920887 1096 blastx.14 argininosuccinate lyase gil2635409 emb CAB 54% 365 1 908245 1105 HMMER PFAM: DEAD and DEAD and DEAD and DEAD and DEAD and DEAD and DEAH box helicases PF00270 72.08 37 1 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 954142 1125 blastx.14 (AJ000758) precorrin-4 gi 3724045 emb CAA 32% 3 2 methylase [Bacillus methylase [Bacillus 04314.1 methylase [Bacillus 32% 3 2					SbcD homolog	6119.1	47%	193	249
920887 1096 blastx.14 argininosuccinate lyase gil2635409[emb CAB 54% 365 1 908245 1105 HMMER PFAM: DEAD and DEAD and DEAD and DEAD and Blastx.14 PF00270 72.08 37 1 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 1 954142 1125 blastx.14 (AJ000758) precorrin-4 gil3724045[emb CAA 32% 3 2 methylase [Bacillus megaterium] megaterium] 24314.1 A7% 56% 5 2					[Rhodobacter capsulatus]				
908245 1105 HMMER PFAM: DEAD and PF00270 72.08 37 1.8 DEAH box helicases 1544.1 66% 5 5 5 5 5 5 5 5 5	HCWEM51	920887	1096	blastx.14	argininosuccinate lyase	gi 2635409 emb CAB	54%	365	39
PFAM: DEAD and DEAD and DEAD and DEAD and DEAH box helicases PFO0270 72.08 37 1.8 DEAH box helicases gi[2443870]gb AAB8 100% 37 blastx.14 (AC002985) R27090_2 gi[2443870]gb AAB8 100% 37 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 954142 1125 blastx.14 (AJ000758) precorrin-4 gi[3724045]emb CAA 32% 3 methylase [Bacillus 04314.1 methylase [Bacillus] 04314.1 an expansional 3					[Bacıllus subtilis]	14904.1	47%	57	7
1.8 DEAH box helicases gi 2443870 gb AAB8 100% 37 blastx.14 (AC002985) R27090_2 gi 2443870 gb AAB8 100% 37 571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 954142 1125 blastx.14 (AJ000758) precorrin-4 gi 3724045 emb CAA 32% 3 methylase [Bacillus 04314.1 methylase [acillus] 04314.1 acillus 32%	HCWEQ14	908245	1105	HMMER	PFAM: DEAD and	PF00270	72.08	37	177
571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 954142 1125 blastx.14 (AJ000758) precorrin-4 methylase [Bacillus megaterium] gi 3724045 emb CAA 32% 3	-			1.8	DEAH box helicases				
571355 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 954142 1125 blastx.14 (AJ000758) precorrin-4 methylase [Bacillus methylase [Bacillus methylase [Bacillus]] 04314.1 32% 3				blastx.14	(AC002985) R27090_2	gi 2443870 gb AAB8	100%	37	177
571355 1116 HMMER PFAM: Heat shock hsp90 PF00183 10.32 37 954142 1125 blastx.14 (AJ000758) precorrin-4 gi 3724045 emb CAA 32% 3 methylase [Bacillus 04314.1 megaterium] megaterium]	1				[Homo sapiens]	1544.1	%99	3	40
954142 1125 blastx.14 (AJ000758) precorrin-4 gi 3724045 emb CAA 32% 3 methylase [Bacillus megaterium] megaterium]	HCWEW45	571355	1116	HMMER	PFAM: Heat shock hsp90	PF00183	10.32	37	186
954142 1125 blastx.14 (AJ000758) precorrin-4 gi 3724045 emb CAA 32% 3 methylase [Bacillus 04314.1 megaterium]	, orthingin			1.8	proteins				
04314.1	HCWEY34	954142	1125	blastx.14	(AJ000758) precorrin-4	gi 3724045 emb CAA	32%	3	242
megaterium]	W				methylase [Bacillus	04314.1			_
					megaterium]				

181	270	152	269	236	288	09	137		158	314	211	301	394	112
140	34	105	105	126	214	137	9		9	195	310	56	341	89
4.92	36.2	4.51	71.4	50.8	4.04	73%	58.7		%98	47%	33%	41%	20%	2.09
PF00018	PF00562	PF00271	PF00171	PF01197	PF00293	pir A37334 A37334	PF00165		gi 148382 gb AAA24 811.1	gi 1736771 dbj BAA1	5920.1	gi 736300 emb CAA8 8644.1	-	PF00130
PFAM: Src homology domain 3	PFAM: RNA polymerase beta subunit	PFAM: Helicases conserved C-terminal	PFAM: Aldehyde dehydrogenase family	PFAM: Ribosomal protein L31	PFAM: Bacterial mutT protein	L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1	PFAM: Bacterial	helix proteins, araC family	operon regulatory protein [Erwinia carotovora]	Nodulation protein V (EC	2.7.3). [Escherichia coli]	Isp42p [Saccharomyces cerevisiae]		PFAM: Phorbol esters / diacylglycerol binding domain
HMMER 1.8	HMMER 2.1.1	HMMER 1.8	HMMER 2.1.1	HMMER 2.1.1	HMMER 1.8	blastx.14	HMMER 1.8	2	blastx.14	blastx.14		blastx.14	-	HMMER 1.8
1143	1149	1186	1196	1217	1223	1262	1288			1295		1305		1334
506577	861907	690751	853005	861843	967067	964088	960159			889026		953384		598510
HCWFF88	HCWFK57	HCWFT29	HCWFU66	HCWGB78	HCWGE12	HCWGW12	HCWGY90			HCWHB12		HCWHD07		HCWHP/4

14	206	126	253	247	218	308	265	148	148	148	148	6	6	252	104	6	6	107	252	160	160	252	107	107	249	15	163	27
85	271	209	300	291	238	141	107	261	327	261	261	122	122	329	157	104	107	142	305	249	249	305	157	157	311	107	246	83
20%	45%	35%	43%	46%	85%	39.4	90.5	57%	45%	20%	20%	36%	34%	61%	55%	40%	33%	%99	55%	26%	79%	44%	41%	41%	33%	22%	32%	57%
gi 4584539 emb CAB	40769.1					PF00795	PF00327	gi 3510629 gb AAC8	0285.1		~		***			•									· · · · · · · · · · · · · · · · · · ·			gi 1335196 emb CAA
(AL049608) extensin-like	protein Arabidopsis	thaliana]				PFAM: Carbon-nitrogen hydrolase	PFAM: Ribosomal protein L30p/L7e	(AF047828) syringomycin	synthetase [Pseudomonas	syringae pv. syringae]											•							pot. ORF I [Homo
blastx.14						HMMER 2.1.1	HMMER 2.1.1	blastx.14					,															blastx.14
1336						1337	1343	1349													·						1000	1388
924187						574945	935419	924105		···-																	00000	939388
НСWНQ03					TOTHINI	нс wнQ31	HCWHR81	HCWHT59				-															UCWIVEOO	IIC WNF US

256	82	179	169	83	258	29	142	43	218	7	282	7	263	345	126	119	315	191	306	3	301	316		134 262
303	192	247	249	148	281	61	219	120	238	240	449	99	126	304	103	99	250	289	326	341	2	2	-	66 182
62%	32%	47%	25%	20%	62%	54%	34%	42%	57%	47%	42%	35%	100%	85%	87%	44%	36%	27%	71%	45%	55.15	42%		43%
26917.1			gi 2109271 gb AAB5	8161.1			gi 6002364 emb CAB	56729.1		gi 887832 gb AAA83	063.1		gi 4104812 gb AAD1	1957.1				gi 3638957 gb AAC3	6301.1	gi 147755 gb AAA24	PF00122	gb AAB37345.1		gi 2622314 gb AAB8 5694.1
sapiens]			CeoB [Burkholderia	cepacia]			(AL121600) hypothetical	protein SCF76.09 1		ORF_0485 [Escherichia	coli]		(AF039571) peripheral	benzodiazepine receptor	interacting protein; PBR-	IP/PRAX1 [Homo	sapiens	(AC004877) sco-spondin-	mucin-like; similar to P98167 1 saniens1	DNA primase Escherichia colil	PFAM: E1-E2 ATPases	cadmium resistance protein [Lactococcus	lactis	(AE000888) malate dehydrogenase [Methanobacterium
			blastx.14		-	,	blastx.14		,	blastx.14		,	blastx.14					blastx.14		blastx.14	HMMER 1.8	blastx.2		blastx.14
		,	1409			!	1427		100	1437		9,	1442				,	1453		1462	1470		,	1516
		00000	085666			100000	108666		00000	765556		20000	960095		_		0.00	959458		965024	853009		00001	958/91
		11/1/1/1/00	HCWNINGS			11/11/11/11/01	HCWKV68		2001 IMOII	HC WLD00		11/1/11/11	HCWLE3/	-			OFIT TITOIT	HCWLH/9		HCWTB11	HCWTB56		TICHT/TEDOO	HCW1KU8

	151 198	2 166	33 77	2 514 537 635			2 997	335 577	363 740	513 716 715 789		48 329 293 397
	6.14	47.52	2.17		100%	ļ	%08	39.1	54.2 3	92% 5		
		4		10	10		∞	3	5	666	5(5.5
	PF00271	PF00389 .	PF00099	gi 4405795 gb AAD1 9826.1		PF00854	gb AAD24570.1 AF1 21080_1	PF01433	PF00621	gi 5020264 gb AAD3 8043.1 AF151363_1	gi 3941737 gb AAC8	gb AAD24570.1 AF1 21080_1
thermoautotrophicum	PFAM: Helicases conserved C-terminal domain	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PFAM: Zinc-binding metalloprotease domain	(AF038963) RNA helicase [Homo sapiens]		PFAM: POT family	(AF121080) cAMP inducible 1 protein [Mus musculus]	PFAM: Peptidase family M1	PFAM: RhoGEF domain	(AF151363) Cdc42 GTPase-activating protein Mus musculus	(AF109719) BAT2 [Mus musculus]	(AF121080) cAMP inducible 1 protein [Mus musculus]
	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.14		HMMER 2.1.1	blastx.2	HMIMER 2.1.1	HMMER 2.1.1	blastx.14	blastx.14	blastx.2
	1517	1519	1593	1633		1646		1655	1678	1694	1736	1737
	729290	654317	661570	926991		941282		947832	794275	974494	926498	741724
	HCWTR54	HCWTS15	HCWUU16	HDDMA83		HDMAQ15		HDPAG32	HDPCN94	HDPFF07	HDPIT53	HDPIT61.

	959653	1750	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041	4.82	340	405
506	909091	1755	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	39.5	280	507
35	582015	1775	blastx.2	(AF038007) FIC1 [Homo sapiens]	gb AAC63461.1	54%	152	703
6	912722	1780	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loon)	PF00071	132.39	127	432
			blastx.2	rab-related GTP-binding	emb CAA68227.1	54%	133	444
10	934520	1788	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	206.63	3	734
			blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA 03387.1	92%	3	734
	792193	1797	HMMER 1.8	PFAM: EF hand	PF00036	7.78	266	313
	812091	1815	HMMER 2.1.1	PFAM: Fes/CIP4 homology domain	PF00611	22.4	151	387
- ·	951276	1818	HMMER 1.8	PFAM: Lectin C-type domain short and long forms	PF00059	37.49	245	376
. .	919404	1837	blastx.14	ORF YGR090w [Saccharomyces cerevisiae]	gi 1323133 emb CAA 97093.1	30%	266	451
- ,	961323	1849	blastx.14	reverse transcriptase [Homo sapiens]	gi[439877]gb AAB02 291.1	66% 37% 54%	280	59 351 267
	722699	1868	HMMER 1.8	PFAM: IG (immunoglobulin)	PF00047	3.32		24

HMMER PFAM: PH (pleckstrin proute) 1.8 homology) domain HMMER PFAM: PH domain 2.1.1 blastx.2 (AF102854) membrane- gblAAD04568.1 associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus] blastx.14 (AF061738) leucine gi[4335941]gb AAD1 aminopeptidase [Homo 7527.1 sapiens] blastx.14 Bat2 [Homo sapiens] gi[29375]emb CAA 76598.1 blastx.14 (AF039571) peripheral gi[4104812]gb AAD1 benzodiazepine receptor interacting protein; PBR- peripheral gi[4104812]gb AAD1 peripheral gi[4104812]gb AAD1 penzodiazepine receptor interacting protein; PBR- peripheral gi[4104812]gb AAD1 penzodiazepine receptor interacting protein; PBR- penzodiazepine receptor interacting protein; PBR- penzodiazepine receptor interacting protein; PBR- penzodiazepine receptor interacting protein; PBR- penzodiazepine receptor interacting protein; PBR- plastx.14 fractionated X-irradiation- gi[1389694[gb AAB0] induced 29 thymoma 2905.1 flattx.2 cverteine rich hair bereatin ambier perenting protein; plastx.2 cverteine rich hair bereatin					superfamily				
1890 HMMER PFAM: PH domain PF00169	96	6556	1877	HMMER. 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	16	518	613
blastx.2 (AF102854) membrane- associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus] 1894 blastx.14 (AF061738) leucine aminopeptidase [Homo 7527.1 sapiens] 1914 blastx.14 Bassoon [Mus musculus] gij3413810 emb CAA 76598.1 1944 blastx.14 (AF039571) peripheral gij4104812 gb AAD1 6bnzodiazepine receptor 1957.1 1945 blastx.14 fractionated X-irradiation- gil1389694 gb AAB0 induced 29 thymoma 2905.1 1946 blastx.2 cvereine rich hair keretin amble A 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	<u> </u>	09916	1890	HMMER 2.1.1	PFAM: PH domain	PF00169	81.2	412	708
2 Maguin-2 [Rattus norvegicus] 1894 blastx.14 (AF061738) leucine gi[4335941]gb AAD1 aminopeptidase [Homo 7527.1] sapiens] 1914 blastx.14 Bat2 [Homo sapiens] gi[29375 emb CAA78 1944 blastx.14 (AF039571) peripheral gi[4104812]gb AAD1 benzodiazepine receptor interacting protein; PBR- 1957.1 1945 blastx.14 fractionated X-irradiation- gi[1389694 gb AAB0 induced 29 thymoma 2905.1 1946 blastx.2 cveterne rich hair keratin gmb/CAA55230.11				blastx.2	(AF102854) membrane- associated guanylate kinase-interacting protein	gb AAD04568.1	36%	349	756
1894 blastx.14 (AF061738) leucine 7527.1 sapiens sapiens 1914 blastx.14 Bassoon [Mus musculus] gi[3413810 emb CAA 76598.1 1944 blastx.14 Bat2 [Homo sapiens] gi[29375 emb CAA78 744.1 1944 blastx.14 (AF039571) peripheral gi[4104812 gb AAD1 197/RAX1 [Homo sapiens] gi[1389694 gb AAB0 1945 blastx.14 fractionated X-irradiation-gi[1389694 gb AAB0 induced 29 thymoma 2905.1 Mus musculus] mathematical part kerating protein, part kerating 2905.1 musculus] mathematical part kerating mathematical part kerating 2905.1 musculus] mathematical part kerating mathematical part kerating 2005.1 mathematical pa					2 Maguin-2 [Rattus norvegicus]				
aminopeptidase [Homo 7527.1] sapiens] 1914 blastx.14 Bassoon [Mus musculus] gij3413810 emb CAA 76598.1 1936 blastx.14 Bat2 [Homo sapiens] gij29375 emb CAA78 744.1 1944 blastx.14 (AF039571) peripheral gij4104812 gb AAD1 benzodiazepine receptor interacting protein; PBR- 1957.1 1945 blastx.14 fractionated X-irradiation- gij1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] 1946 blastx.2 cveteine rich hair kerzetin gmblCAA65230.11	<u> </u>	915964	1894	blastx.14	(AF061738) leucine	gi 4335941 gb AAD1	94%	3	152
1914 blastx.14 Bassoon [Mus musculus] gi[3413810 emb CAA 76598.1 1936 blastx.14 Bat2 [Homo sapiens] 744.1 1944 blastx.14 (AF039571) peripheral gi[4104812 gb AAD1 benzodiazepine receptor 1957.1 197PRAX1 [Homo sapiens] 1945 blastx.14 fractionated X-irradiation- gi[1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] contribusir keratin comblex A 65230.11					aminopeptidase [Homo	7527.1	87%	316	438
1914 blastx.14 Bassoon [Mus musculus] gi[3413810 emb CAA 76598.1 1936 blastx.14 Bat2 [Homo sapiens] 744.1 1944 blastx.14 (AF039571) peripheral gi[4104812]gb AAD1 penzodiazepine receptor 1957.1 1947 blastx.14 fractionated X-irradiation-gi[1389694 gb AAB0 induced 29 thymoma 2905.1 fMus musculus] musculus] musculus					sapiens		%08	140	217
1914 blastx.14 Bat2 [Homo sapiens] 76598.1 76598.1 1936 blastx.14 Bat2 [Homo sapiens] 744.1 744.1 1944 blastx.14 (AF039571) peripheral gil4104812[gb AAD1 benzodiazepine receptor 1957.1 1P/PRAX1 [Homo sapiens] 1945 blastx.14 fractionated X-irradiation- 2905.1 Mus musculus] 1946 blastx.2 cverteine rich hair keratin 2905.1 2946 blastx.2 cverteine rich hair keratin 2905.1 2946 blastx.3 2005.1 2005.1							%56	254	316
1914 blastx.14 Bassoon [Mus musculus] gi 3413810 emb CAA 76598.1 1936 blastx.14 Bat2 [Homo sapiens] 744.1 1944 blastx.14 (AF039571) peripheral gi 4104812 gb AAD1 benzodiazepine receptor interacting protein; PBR- 1957.1 1P/PRAX1 [Homo sapiens] sapiens] [IP/PRAX1 fractionated X-irradiation- gi 1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] cysteine rich hair keratin gmb CAA65230.1							62%	425	472
1914 blastx.14 Bassoon [Mus musculus] gij3413810 emb CAA 76598.1 1936 blastx.14 Bat2 [Homo sapiens] gi]29375 emb CAA78 744.1 1944 blastx.14 (AF039571) peripheral gi 4104812 gb AAD1 19677.1	_1	, 00000	,				33%	305	358
1936 blastx.14 Bat2 [Homo sapiens] gi 29375 emb CAA78 1944 blastx.14 (AF039571) peripheral gi 4104812 gb AAD1 benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens] 1945 blastx.14 fractionated X-irradiation- gi 1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] 2965.1 2946 blastx.2 exsteine rich hair keratin amb CAA66220.1		927024	1914	blastx.14	Bassoon [Mus musculus]	gi 3413810 emb CAA 76598.1	75%	239	216
1944 blastx.14 (AF039571) peripheral gi 4104812 gb AAD1 benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens] sapiens] 1945 blastx.14 fractionated X-irradiation- gi 1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] cysteine rich hair keratin ambl/A A 56220.11		909848	1936	blastx.14	Bat2 [Homo sapiens]	gi 29375 emb CAA78 744.1	37%	248	201
benzodiazepine receptor 1957.1 IP/PRAX1 [Homo sapiens] sapiens] 1945 blastx.14 fractionated X-irradiation- gil1389694[gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] Systeme rich hair keratin supply A A 5622.0.1		963481	1944	blastx.14	(AF039571) peripheral	gi 4104812 gb AAD1	28%	490	455
interacting protein; PBR- IP/PRAX1 [Homo sapiens] 1945 blastx.14 fractionated X-irradiation- induced 29 thymoma [Mus musculus] [Mus musculus] cysteine rich hair keratin amhl/A A 56230 11					benzodiazepine receptor	1957.1	43%	387	319
1945 blastx.14 fractionated X-irradiation-gi[1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] cysteine rich hair keratin ambl(7 A 56220.1)		•			interacting protein; PBR-		100%	9/	59
1945 blastx.14 fractionated X-irradiation-gi[1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] cysteine rich hair keratin amh[CAA65220.1]					IP/PRAX1 [Homo		55%	253	227
1945 blastx.14 fractionated X-irradiation- gi[1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] 1946 blastx.2 cysteine rich hair keratin ambl/CAA 56230.11					sapiens]		42%	256	215
1945 blastx.14 fractionated X-irradiation- gi 1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] 1946 blastx.2 everteine rich hair kerstin ambl/CAA 56220.11							28%	45	10
1945 blastx.14 fractionated X-irradiation- gi 1389694 gb AAB0 induced 29 thymoma 2905.1 [Mus musculus] 1946 blastx 2 cysteine rich hair keratin ambl/CAA 56230.11	- 1	700,0	1				83%	51	34
Induced 29 thymoma 2905.1 [Mus musculus] [Ads blastx 2 cysteine rich hair keratin amble A 8 5 6 2 2 0 1]	٠,	01336	1945	blastx.14	fractionated X-irradiation-	gi 1389694 gb AAB0	51%	47	256
1946 blastx 2 exertine rich hair kerstin amble A 56220 11	- 1				induced 29 thymoma [Mus musculus]	2905.1	71%	2	43
System Specific from the Child CAA 30334.1	\sim 1	379416	1946	blastx.2	cysteine rich hair keratin	emb CAA56339.1	40%	65	319

											
352	. 254	255 371 403	347	248 356 464	297	302	170	233	354	326	350
99	78	330	159	132 273 357	163	3	192	180	244	108	36
42%	%86	98% 85% 100%	18.53	58% 75% 58%	29.85	93.6	35%	7.98	78%	31.58	65%
	gi 3800869 gb AAC6 8900.1	gi 3800869 gb AAC6 8900.1	PF00047	emb CAA08796.1	PF00085	PF00069	gi 1517820 gb AAC5 0918.1	PF00125	gi 919 emb CAA3980 0.11	PF00076	gb AAA35554.1
associated protein [Oryctolagus cuniculus]	(AF086624) serine threonine kinase [Rattus norvegicus]	(AF086624) serine threonine kinase [Rattus norvegicus]	PFAM: IG (immunoglobulin) superfamily	(AJ009698) embigin protein [Rattus norvegicus]	PFAM: Thioredoxins	PFAM: Eukaryotic protein kinase domain	p56 KKIAMRE protein kinase [Homo sapiens]	PFAM: Core histones H2A, H2B, H3 and H4	rab4b [Canis familiaris]	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	arginine-rich nuclear
	blastx.14	blastx.14	HMMER 1.8	blastx	HMMER 1.8	HMMER 2.1.1	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	blastx.2
	1956	9561	1959		1968	1973		1977	1984	1987	
	973925	974565	945083		846630	934472		916348	912765	964709	
	HDTAY23	HDTAY23	HDTB048		HDTBR50	HDTBY88		HDTDC53	HDTEI19	HDTES50	

	612	168	101	216	49	49	371	430	389	341	341	389	344	356	344	674	320	554	245	457	547	553	457	442	554	524
	4	100	45	172	2	5	318	407	45	45	33	45	45	48	45	18	18	09	18	347	347	338	374	338	519	315
	97%	43%	42%	46%	43%	40%	38%	7.07	46%	53%	20%	45%	47%	49%	46%	33%	42%	34%	21%	27%	37%	32%	20%	47%	%99	61%
	gi 1665781 dbj BAA1 3387.1	gi 3638957 gb AAC3	6301.1					PF00096	dbj BAA92059.1																	gb AAC08737.1
nrotein [Homo saniens]	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) [Homo sapiens]	(AC004877) sco-spondin-	mucin-like; similar to	P98167 1 sapiens]				PFAM: Zinc finger, C2H2 type	(AK002053) unnamed	protein product [Homo	sapiens]															(AF010144) neuronal
	blastx.14	blastx.14						HMMER 1.8	blastx.2						142.40										,	blastx.2
	2009	2012						2016				20.52													1	2017
	923899	699256		******		·		908946																		8830/0
	НОТНQ15	HDTHZ46			****	***************************************		HDTID61								-									TIP GITTO	HD11F01

				thread protein AD7c-NTP		61%	309	509
		.,,,,		[Homo sapiens]		65%	361	507
						62%	34	162
						%09	53	172
						41%	304	507
		-,-,				35%	286	507
						40%	327	473
			-	PAT		20%	50	151
						21%	68	166
						47%	109	171
						37%	308	379
PY 77 4 4	1 2 0 0					52%	128	178
HD 11244	97557/4	2032	blastx.14	procollagen alpha 2(V)	gi 2370202 emb CAA	43%	77	6
				[Homo sapiens]	75002.1	40%	68	6
						37%	68	6
						21%	229	188
						47%	183	133
						%09	135	106
						47%	328	278
						75%	165	142
					123	%09	121	92
			***************************************			43%	139	92
						54%	165	133
						\ \%09	162	133
TION	70000	000	1			54%	226	194
HD1315/	/99834	2036	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	2.02	386	466
HDTJJ02	913787	2037	HMIMER	PFAM: Phorbol esters /	PF00130	5.7	21	89
			1.0	diacylglycerol binding domain				
HDTKQ14	986938	2044	HMMER	PFAM: Src homology	PF00018	12.87	430	546
		i		7.0	-	177.01	りたよ	

			1.8	domain 3				
			blastx.2	(AL049683) hypothetical	emb CAB41255.1	100%	439	555
				protein [Homo sapiens]		26%	9/	291
HDTLD17	908601	2052	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	96.3	154	222
			blastx.2	Zfp-29 [Mus musculus]	emb CAA38920.1	48%	49	636
	-					65%	49	399
-					,	%99	49	399
						%99	70	399
						92%	49	411
						62%	49	369
						64%	70	381
						47%	115	989
1						28%	49	324
						42%	372	641
						20%	375	695
						47%	375	995
						47%	375	995
						48%	372	569
						43%	372	578
···						42%	372	605
						46%	375	995
						35%	279	569
***************************************						43%	372	569
						43%	375	569
				-		46%	375	695
						63%	547	989
						63%	547	989
						52%	538	651
						26%	547	642
						35%	375	491

299	428	303	228	92	41	148	437	246	173	207	210	 : i			198	2		230	91	233	9	174	241	312	533	629
641	460	338	290	154	82	219	294	136	129	172	10	9			320	1		274	129	271	44	206	44	247	213	6
%99	63%	20%	33%	38%	. 20%	29%	%02	40%	93%	83%	52%		_		29%			53%	38%	53%	30%	27%	46%	20%	42.5	%96
	gi 1869859 emb CAB	06722.1					gi 1825586 gb AAB4	2222.1	gi 3043919 gb AAC1	3265.1	gi 4426837 gb AAD2	0564.1			gi[179339]gb AAA35	585.1		gi 1247469 emb CAA	01862.1				pir(B25313 GNLRL1		PF00169	emb CAB65966.1
	very large tegument	protein [human	herpesvirus 2]				contains similarity to C2	domains [Caenorhabditis elegans]	(AF034970) docking	protein Homo sapiens]	(AF108420) 1-	aminocyclopropane-	carboxilate synthase	[rugu rubripes]	HLA-B-associated	transcript 2 (BAT2)	[Homo sapiens]	TGR-CL5bis [Homo	sapiens]				retrovirus-related reverse	transcriptase pseudogene - slow loris	PFAM: PH domain	(AJ250425) Collybistin I
	blastx.14						blastx.14		blastx.14		blastx.14				blastx.14			blastx.14					blastx.14		HMIMER	blastx.2
	2091						2092		2113		2118				2121			2131					9562		2142	
	963338		·			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	920911		959581		936687				006596			919200					961148		930705	
OF COURT	HEOMG48					0000	HEOMG/8		HEOMS08		HEOMI79			Out to Court	HEOMU79			HEOMX92		-1		COLEN COLLEGE	HEOMX92		HEONQ19	

279	364	111	346	334	250	134	237	609	609	480	306	582	1026	152	145	145	267	325	84	206	264	81	203	325
163	320	142	429	429	273	208	169	139	139	139	154	196	250	30	101	101	232	284	58	180	223	28	180	302
51%	5.32	38%	32%	31%	75%	36%	6.98	37%	33%	35%	52%	29%	420.7	21%	53%	46%	20%	%05	55%	55%	42%	62%	62%	62%
dbj BAA91707.1	PF00099	gi 214044 gb AAA49	679.1				PF00096	dbj BAA91884.1					PF00144	gi 475909 emb CAA4 7472.1	gi 1732471 gb AAB4	9656.1								
(AK001463) unnamed protein product [Homo sapiens]	PFAM: Zinc-binding metalloprotease domain	alpha-1 type II collagen	[Xenopus laevis]				PFAM: Zinc finger, C2H2 type	(AK001753) unnamed	protein product [Homo	sapiens]			PFAM: Beta-lactamase	ORF1A [Homo sapiens]	rehydrin [Tortula ruralis]									
blastx.2	HMMER 1.8	blastx.14					HMMER 2.1.1	blastx.2					HMMER 2.1.1	blastx.14	blastx.14									
2148	2157	2174			_		2189						2203	2204	2214									
949152	851009	958184					909032		······································				942596	965930	959572									
HEONV59	HEOPE58	HEOPO08					HEOQC76 						HEOQP44	HEOQS11	HEORE79									

174	1801	156	417	114	114 297	06	708	288	421	448	186	144
302	1202	115	226	25	235	64	526	88	233	212	103	13
65%	99%	4.1	95%	12.86	52%	3.27	30.41	11.81	166.4	%68	10.48	%09
gi[3170182 gb AAC1 8040.1	gi 5881961 gb AAD5 5138.1 AF064257 1	PF00130	gi 5823554 gb AAD5 3184.1 AF180920_1	PF00035	gi 158506 gb AAA73 062.1	PF00130	PF00018	PF00183	PF01352	gi 506502 emb CAA5 6225.11	PF00435	gi 5689158 dbj BAA8 2838.1
(AF039691) antigen NY- CO-9 [Homo sapiens]	(AF064257) Dhm1-like protein [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding domain	(AF180920) cyclin ania- 6a [Homo sapiens]	PFAM: Double-stranded RNA binding motif	[D.melanogaster mRNA, complete cds.], gene product [Drosophila	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Src homology domain 3	PFAM: Heat shock hsp90 proteins	PFAM: KRAB box	NK10 [Mus musculus]	PFAM: Spectrin alpha chain, repeated domain	(AB023622) Septin6 [Mus musculus]
blastx.14	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER 2.1.1	blastx.14	HMMER 1.8	blastx.14
2250	2267	2279	2282	2302	· ·	2346	2354	2381	2392		2400	
915285	952455	923895	961974	919630		871911	932851	783820	298867		965709	
HHECO01	HHEEC07	ннен073	ннелнзо	HHEND45	and the second	ННЕОК01	ннедv39	HHESU85	HHETQ54		HHEUA62	

92	37	782	123		123	372		340	104			284		330	6	162	176	203	124	317	115	72	317	352
3	11	129	82			277		107	3			264		440	47	115	165	174	189	355	189	107	349	387
31.5	2.17	95%	1.99		48.1	78%		82%	100%			2.86		%68	%69	43%	100%	70%	20%	61%	44%	28%	63%	20%
PF00023	PF00099	gi 5059425 gb AAD3 9005.1 AF156884 1	PF00130		PF01449	gi 5020264 gb AAD3	8043.1 AF151363_1	gi 1651236 dbj BAA3	5202.1			PF00099		gi 2766165 dbj BAA2	4267.1	gi 334072 gb AAA47	471.1		gi 159657 gb AAA29	371.1				
PFAM: Ank repeat	PFAM: Zinc-binding metalloprotease domain	(AF156884) RIP-like kinase [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding	domain	PFAM: Phosphate- binding protein	(AF151363) Cdc42	GTPase-activating protein [Mus musculus]	Hypothetical	bacteriophage n4 receptor	protein NfrA precursor.	Escuencina con	PFAM: Zinc-binding	metalloprotease domain)EP	[Homo sapiens]	ORF-3 protein	[Pseudorabies virus]		collagen [Ascaris suum]					
HIMMER 2.1.1	HMMER 1.8	blastx.14	HMMER 1.8	477 67 411	HMMEK 2.1.1	blastx.14		blastx.14				HMMER	1.8	blastx.14		blastx.14			blastx.14	_			_	
2401	2486	2526	2529	02.20	25/2	2600		2633				2641		2679		2694			2697					
795268	963724	950728	531053	571770	231228	999606		969296				531054		950096		920292			932127					
HHEUC31	HKBAT27	HLMBW11	HLMBY16	111 141171	HLMD0/1	HLMFU09		HLMHP67				HLMHT94		HLMIX95		HLMMA52			HLMMD05					

317	366	317	99	115	317	322	382	384	448	419	256	146	138	231	280	153	57	208	260	15	158	293	191	215	156	182	3
358	407	355	110	189	355	245	230	337	404	378	173	66	61	184	345	191	98	306	162	68	229	376	259	283	179	232	76
42%	20%	46%	46%	32%	46%	17.86	62%	81%	%98	71%	39%	43%	%01	37%	36%	53%	20%	33%	37.3	44%	37%	35%	30%	39%	75%	47%	75%
er eterstelle de de de de de de de de de de de de de						PF00023	gi 488505 dbj BAA06	418.1					gi 687206 gb AAA63	589.1	914494984 9h AAD2	1406.1	_		PF00169	gi 334072 gb AAA47	471.1	.10 2 2		-			•
						PFAM: Ank repeat	similar to HUMORFU	(D26069) [Homo sapiens]					dynein heavy chain	isotype 6 [Tripneustes	(AF083501) latent nuclear	antigen [Macaca mulatta	rhadinovirus 17577]		PFAM: PH domain	ORF-3 protein	[Pseudorabies virus]						
						HMMER 1.8	blastx.14						blastx.14		blastx.14				HMMER 2.1.1	blastx.14							
						2733							2769		2776				2871	2980							
						926188							964739		920296				909874	998606							
						HLMMV66							HLMNL55		HLMNN02				HLYAA41	HLYDL60							

197	3 161	3) 124	3 406	504	409	74	234		231	403	
	223	200	68	188	113	383	12	1 264	347	157	281 154 233	210
38%	38%	%68	4.11	58.6	41%	2.86	24.4	65%	100%	24.8	39% 56% 61%	128.8
		gi 473842 gb AAA20 666.1	PF00096	PF00169	gb AAC35236.1	PF00130	PF00612	sp BAA33720 BAA3 3720	gi 1651427 dbj BAA3 5638.1	PF00025	gi 3746799 gb AAC6 4063.1	PF00204
		orfIV [Borna disease virus]	PFAM: Zinc finger, C2H2 type	PFAM: PH domain	(AC005496) unknown protein [Arabidopsis thaliana]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: IQ calmodulin- binding motif	EDTP(egg derived tyrosine phosphatase).	Formate c-acetyltransferase (EC 2.3.1.54). [Escherichia coli1	PFAM: ADP-ribosylation factor family	(AF082517) ADP-ribosylation factor Entamoeba histolytical	PFAM: DNA topoisomerase II (N-terminal region)
		blastx.14	HMMER 1.8	HMMER 2.1.1	blastx.2	HMMER 1.8	HMMER 2.1.1	blastx.14	blastx.14	HMMER 2.1.1	blastx.14	HMMER 2.1.1
		2986	2991	2993		3005	3042	3056	3062	3063		3065
		966732	526245	927872		682176	832311	920551	968199	907640		729831
		HL YDS11	HLYDT68	HLYDV62		HL YEN93	HLYGP46	HLYHN67	HMAAF10	HMABJ56		HMABQ71

143	728	303	405	402	390	112	422	803	1545	1474	296	456	573	168	320	187	423	58	122	132	183
202	270	46	31	115	112	2	363	1516	1673	1587	63	85	445	10	183	119	313	5	06	7	166
%56	%86	06	40.87	62.9	84%	100%	25%	%66	%06	20%	50.17	82%	%06	71%	73%	82%	43%	61%	63%	51.9	3.49
gi 536985 gb AAA97 040.1	dbj BAA92041.1	PF00568	PF00512	PF01432	gi 466635 gb AAB18	474.1		gi 1480003 dbj BAA1	1058.1		PF00406	emb CAB59367.1			pir S72481 S72481					PF01344	PF00099
ORF_f418 [Escherichia coli]	(AK002022) unnamed protein product [Homo sapiens]	PFAM: WH1 domain	PFAM: Signal C termial domain	PFAM: Peptidase family M3	CG Site No. 18031	[Escherichia coli]		MaoB [Escherichia coli]			PFAM: Adenylate kinases	(AJ007798) stromal	antigen 3, (STAG3)	[Homo sapiens]	probable transposase -	human transposon MER37				PFAM: Kelch motif	PFAM: Zinc-binding
blastx.14	blastx.2	HMMER 2.1.1	HMMER 1.8	HMMER 2.1.1	blastx.14			blastx.14			HMMER 1.8	blastx.2			blastx.14					HMMER 2.1.1	HMMER
3067	3071	3078	3080	3085				6956			3091	3107			3110					3117	3127
920088	939916	778521	723186	947905				966282			956195	895981			963794					753133	462502
HMADC02	HMADZ55	HMAFY42	HMAGK69	HMAIC22				HMAKA11			HMALL66	HMCDN22			HMCFB22					HMCGY77	HMMAB49

			1.8	metalloprotease domain				
HMMAC19	953580	3129	blastx.14	(AF003535) ORF2-like	gi 2197085 gb AAD0	47%	26	145
				protein [Homo sapiens]	4635.1	47%	282	344
						87%	187	210
HMMCH04	944069	3208	blastx.2	unknown [Homo sapiens]	gb AAC50940.1	28%	423	089
HMQBU96	765162	3247	HMMER	PFAM: Helix-loop-helix	PF00010	7.33	8	40
111 (0) 710	,0,0,0	1,00	0.7	DINA-binding domain				
HMQDZ19	940694	3267	blastx.14	urokinase plasminogen	gi 433901 emb CAA5	100%	68	124
			***	activator receptor [Homo sapiens]	2191.1	91%	133	168
HMSBV28	970579	3303	blastx.14	YKL249 [Saccharomyces	gi 871536 emb CAA4	92%	260	108
				cerevisiae]	9304.1	21%	141	ī
						20%	323	282
HMSCD15	918133	3310	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
		~	blastx.2	(AK000975) unnamed	dbi BAA91451.1	%86	453	635
				protein product [Homo	-	762	387	479
				sapiens]		28%	80	175
HMSFR69	738588	3373	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.78	258	202
HMSGL27	855759	9573	HMMER 1.8	PFAM: Bacterial mutT	PF00293	5.56	276	202
HMSGP73	925385	3401	blastx.14	(AC004490) R29381_1 [Homo saniens]	gi 2995577 gb AAC0 8316.11	94%	141	908
HMSGX14	871492	3413	HMMER 1.8	PFAM: Ribosomal protein S12	PF00164	33.44	28	153
HMSHO64	746582	3431	HMMER 1.8	PFAM: Src homology domain 3	PF00018	11.08	316	405
			blastx.2	(AF030131) Plenty of SH3s; POSH [Mus	gb AAC40070.1	47%		411

	208 228	667 1137 241 465		 139 465	2 163	97 513	2 232			302 463	462 527	532 558		365 463		73 256			1252 1329		19 84	99 233
	4.89		21% 2	 16%	48.7	97%	%9/			64% 3	63% 4	88% 5	48% 5		36% 2		26% 5		13.38 12		20%	33%
	4	2 2	7		—–– 4	6	7			9	·9	8	4	 	<u>~</u>	36	7		13	1	5(3,
	PF00098	gi 5669894 gb AAD4 6501.1 AF148805 6			PF01426	gi 3820614 gb AAC6 9630.1	gi 3929219 gb AAC7	9841.1		gb AAF22026.1 AF1	18094_21		gi 3879085 emb CAA	94301.1					PF00125		gi 9300 emb CAA494	72.11
musculus	PFAM: Zinc finger, CCHC class	(AF148805) latent nuclear antigen [Kaposis sarcoma-	associated herpesvirus]		PFAM: BAH domain	(AF094516) E1-like protein [Homo sapiens]	(AF082556) TRF1-	interacting ankyrin-related	ADF-ribose polymerase [Homo sapiens]	(AF118082) PRO1902	[Homo sapiens]		cDNA EST	EMBL:M89462 comes	from this gene; cDNA	EST 1 1 yk349d7.5 comes	from this gene; cDNA	EST yk358b9.5 comes	PFAM: Core histones	H2A, H2B, H3 and H4	Emf1 alpha [Ephydatia	muelleril
	HMMER 1.8	blastx.14			HMMER 2.1.1	blastx.14	blastx.14			blastx.2			blastx.14						HMMER	1.8	blastx.14	
	3447	3491			3498	3509	3538		_	9578			3548						3589		9098	
	733386	200596			744990	959413	958216		_	948130			948202						904807		924634	
	HMSHZ56	HMSJT11			HMSJW19	HMSKI08	HMSOM08			HMSOU92			HMSOX47						HMVDU16		HMWCQ09	

						38%	292	345
HMWDD54	932261	3610	blastx.14	(AF175223) SANT domain protein SMRTER [Drosophila melanogaster]	gi 5815245 gb AAD5 2614.1 AF175223_1	53%	122	84
HMWDF88	692906	3612	HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class A	PF00057	41.61	171	245
			blastx.14	(AF110520) NG29 [Mus	gi 4050096 gb AAC9	%69	114	239
		_		musculus]	7969.1	48%	129	239
						35%	6	110
						20%	72	107
HMWGG55	920575	3642	blastx.14	DNA polymerase [Pyrococcus furiosus]	gi 216918 dbj BAA02 362.1	94%	195	308
HMWGT07	953454	3645	blastx.14	(AL078579) putative	gi 4972120 emb CAB	40%	218	322
				protein [Arabidopsis	43977.1	40%	395	475
				thaliana		46%	113	157
HMWHN70	851334	3654	HMMER	PFAM: Zinc finger,	PF00097	6.51	187	255
	···		1.8	C3HC4 type (RING finger)				
HNEBJ08	958742	3689	blastx.14	mucin 2 precursor,	pir A49963 A43932	35%	305	264
			:	intestinal - human (fragments)		83%	320	303
HINEDU01	909832	3748	blastx.14	(AC002398) F25965_3	gi 2477513 gb AAB8	71%	207	323
				[Homo sapiens]	1198.1	21%	08	205
						62%		87
						43%	323	412
						20%	337	384
HINFEF95	971171	3792	blastx.14	ORF_0493 [Escherichia	gi 606260 gb AAA58	%86	548	201
				coli]	123.1	%68	103	20
	,					81%	185	105
HNFFM25	705856	3818	HMMER	PFAM: Laminin B	PF00052	0.47	520	603

			1.8	(Domain IV)				
HNFFT62	574623	3828	HMMER 1.8	PFAM: C2 domain	PF00168	2.74	207	272
HNFGI01	921431	3851	blastx.14	(AF118890) s-tomosyn isoform [Rattus	gi 4689231 gb AAD2 7819.1 AF118890_1	86%	234	302 200
HNFGI49	2009707	3852	blastx.14	(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	100%	1 09	45
HNFGM76	599806	3862	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	74.8	232	306
	,		blastx.2	(AF132599) RANTES factor of late activated T lymphocytes-1 [Homo sapiens]	gb AAD26864.1 AF1 32599_1	92%		417
HNFHA11	967520	3874	HMMER 2.1.1	PFAM: Phosphoenolpyruvate carboxykinase	PF01293	118.1	55	219
	:		blastx.14	phosphoenolpyruvate carboxykinase [Escherichia coli]	gi 606337 gb AAA58 200.1	%66	55	360
HNFHK77	576186	3890	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	30.2	231	326
HNFHQ01	938114	3897	blastx.14	serine/threonine kinase with SH3 domain, leucine 1	gi 758593 emb CAA8 8531.1	28% 46% 46% 25%	248 43 371 79	331 81 415 186
HNFHW14	939763	3908	HMMER 2.1.1	PFAM: Latrophilin/CL-1- like GPS domain	PF01825	35.1	44	196

			blastx.2	(AF166382) serpentine recentor [Mus musculus]	gb AAF00617.1 AF1 66382 1	44%	38	283
HNFIG07	918389	3921	blastx.14	(AF128881) PI3 kinase	gi 4928058 gb AAD3	%08	2	445
				regulatory subunit P101 [Homo sapiens]	3397.1 AF128881_1	%09	448	477
HNFIP50	965283	3936	blastx.14	mutant sterol regulatory	gi 841318 gb AAA85	65%	356	631
		***		element binding protein-2	718.1	34%	42	128
				1		85%	999	685
HNGAL92	953889	3976	blastx.14	phosphatidylserine decarboxylase	gi 551827 gb AAA83 896.1	73%	212	18
				[Escherichia coli]				
HNGAS51	773208	3984	HMMER	PFAM: Zinc-binding	PF00099	2.57	144	182
			1.8	metalloprotease domain				
HNGBF80	574475	4001	HMMER	PFAM: Zinc finger, C2H2	PF00096	4.98	88	111
			1.8	type				
HNGBH77	577361	4005	HMMER	PFAM: ATP synthase A	PF00119	18.6	130	189
			1.8	chain				
HNGCE85	970738	4039	blastx.14	hypothetical protein	pir S72489 S72489	72%	284	210
	ø			Tigger 2 - human		63%	212	180
				transposon MER37 1				
HNGCX07	953900	4065	HMMER	PFAM: Src homology	PF00018	3.68	45	161
			1.8	domain 3				
HNGEN37	663955	4160	HMMER	PFAM: Indole-3-glycerol	PF00218	125.4	2	223
			2.1.1	phosphate synthases			·	
HNGEQ07	953647	4169	HMMER 1.8	PFAM: TPR Domain	PF00515	10.86	164	238
HNGER43	699391	4173	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	3.79	151	195
HNGER96	952396	4177	blastx.14	Bkm-like protein	gi 552132 gb AAA28	%09	250	294
				[Drosophila melanogaster]	872.1	64%	250	291

						64%	250	291
HNGEW76	572874	4198	HMMER 1.8	PFAM: Helicases conserved C-terminal	PF00271	4.66	194	247
HNGEX35	959230	4200	blastx.14	adenine phosphoribosyltransferase [Escherichia coli]	gi 1773151 gb AAB4 0223.1	%86	205	366
HNGEX95	572897	4202	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	5.32	196	219
HNGFG22	573084	4224	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	9.2	166	240
HNGFG69	926873	4227	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	44% 40% 40% 50%	228 145 145 307 67	175 80 80 80 248
HNGFK28	544726	4234	HMMER 1.8 blastx.2	PFAM: ABC transporters MsbA protein. Escherichia colil	PF00005 dbj BAA35658.1	86.07	445	654 651 651
HNGFK28	566798	9584	HMMER 1.8 blastx.2	PFAM: ABC transporters MsbA protein. Escherichia colil	PF00005 dbj BAA35658.1	86.07	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	654
HNGFK28	943114	9585	HMMER 1.8 blastx.2	PFAM: ABC transporters MsbA protein.	PF00005 dbj BAA35658.1	117.67	342	503

162	37	242	512	10	87	161	198	215	290	422	75		155	129	129	—	129	306	132	132	167	164	248	63	129	129
25	2	3		84	116	205	263	84	102	96			196	167	155	75	152	335 (152	152	196	196	289	131	152	152
84%	91%	6.09	%66	44%	%09	40%	36%	42.7	55.68	44%	%09		%05	53%	%99	36%	75%	09	85%	85%	%09	54%	20%	79%	62%	75%
		PF00664	dbj BAA35658.1	pir S28303 S28303				PF00665	PF00075	gi 930259 emb CAA3	3367.1		gi 1877435 gb AAB5	1499.1											-	
[Escherichia coli]		PFAM: ABC transporter transmembrane region	MsbA protein. Escherichia colil	hypothetical protein	T23G5.2 - Caenorhabditis	elegans		PFAM: Integrase core domain	PFAM: RNase H	reverse transcriptase (476	AA) [Woolly monkey	sarcoma virus]	180 kDa bullous	pemphigoid antigen 2/type	XVII collagen [Homo	sapiens]									,	
		HMMER 2.1.1	blastx.2	blastx.14				HMMER 2.1.1	HMMER 1.8	blastx.14			blastx.14		_		_	•		-					_	
	1	9856	<u> </u>	4244			- 1	4246	4265				4270	•												
		943115		935135				526792	971170				924693													
	COLLEGE	HNGFK28		HNGF046				HNGFO81	HNGFU12				HNGFW09													

type VII collagen gij388625[gb AAA36 66% 66% 66% [Cricetulus griseus] 968.1 42% 42% 42% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50						75%	152	129
type VII collagen gij388625 gb AAA36 60% [Cricetulus griseus] 968.1 968.1 42% PFAM: Laminin B PF00052 50% Somin IV) PFAM: Zinc finger, C2H2 PF00096 6.36 type unknown protein [Homo gi]1196398 gb AAA8 50% sapiens] 0RF2 [Rattus norvegicus] gij56588 emb CAA37 50% collagen type VII [Homo gi]495866 gb AAA58 55% sapiens] 965.1 57% G4% Sapiens] 965.1 645.1 DF000A0 6.75						%99	155	129
type VII collagen gij388625[gb AAA36 50% 50% [Cricetulus griseus] 968.1 42% 42% 508.1 508.1 42% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50						%99	155	129
type VII collagen gij388625 gb AAA36 50% [Cricetulus griseus] 968.1 42% 40% 50% 50% PFAM: Laminin B PF00052 0.51 Omain IV) PFO0096 6.36 type 6.36 50% unknown protein [Homo gi]1196398 gb AAA8 50% sapiens] 8020.1 57% ORF2 [Rattus norvegicus] gi[55588 emb CAA37 50% 645.1 57% collagen type VII [Homo gi[495866 gb AAA58 58% sapiens] 965.1 47% pFAM: PFAM: 57% collagen type VII [Homo gi[495866 gb AAA58 55% sapiens] 965.1 47% collagen type VII [Homo gi[495866 gb AAA58 55% sapiens] 62% sapiens] 62% collagen type VII [Homo 62%						%09	193	164
[Cricetulus griseus] 968.1 34% 42% 40% 50% 58	4306		blastx.14	type VII collagen	gi 388625 gb AAA36	20%	356	397
42% 40% 50% 50% 50% 50% 50% 50% 50% 50% 50% 5				[Cricetulus griseus]	968.1	34%	47	115
PFAM: Laminin B PFAM: Laminin B PFAM: Laminin B PFAM: Laminin B PFAM: Laminin B PFAM: Laminin B PFAM: Laminin B PFO0052 (Domain IV) PFAM: Zinc finger, C2H2 PF00096 (a) 51 (b) 636 unknown protein [Homo gi]1196398 gb AAA8 50% sapiens] (c) 645.1 (c) 6486						42%.	285	341
S9% S8%						40%	288	347
PFAM: Laminin B						20%	171	206
Second Second						28%	171	206
PFAM: Laminin B PF00052 0.51 (Domain IV) PFAM: Zinc finger, C2H2 PF00096 6.36 type unknown protein [Homo gil1196398 gb AAA8 50% sapiens] ORF2 [Rattus norvegicus] gil5588 emb CAA37 50% collagen type VII [Homo gil495866 gb AAA58 55% sapiens] orange of the collagen type VII [Homo gil495866 gb AAA58 55% sapiens] pFAM: Laminin B PF00052 0.51 gil495866 gb AAA8 50% 64% 64% 65% PFAM: DE00040						38%	9	59
PFAM: Laminin B						41%	53	103
PFAM: Laminin B PF00052 0.51 (Domain IV) (Domain IV) 6.36 PFAM: Zinc finger, C2H2 PF00096 6.36 type (all 196398 gb AAA8 50% unknown protein [Homo sapiens] (all 1196398 gb AAA8 50% ORF2 [Rattus norvegicus] (all 5588 emb CAA37 50% collagen type VII [Homo gi 495866 gb AAA58 58% sapiens] 965.1 47% 64% 57% Sapiens] 965.1 47% BFAM: BE00040 62%						20%	171	206
PFAM: Zinc finger, C2H2 PF00096 6.36 type	4317		HMMER	PFAM: Laminin B	PF00052	0.51	424	441
PFAM: Zinc finger, C2H2 PF00096 6.36 type unknown protein [Homo gi 1196398 gb AAA8 50% sapiens] 8020.1 57% ORF2 [Rattus norvegicus] gi 56588 emb CAA37 57% collagen type VII [Homo gi 495866 gb AAA58 58% sapiens] 965.1 47% PFAM: 62% DFAM: DF00040	1		0.1	(Domain I V)				
unknown protein [Homo gi 1196398 gb AAA8 50% sapiens] 8020.1 50% ORF2 [Rattus norvegicus] gi 56588 emb CAA37 50% 645.1 57% collagen type VII [Homo gi 495866 gb AAA58 58% sapiens] 965.1 55% PFAM. PFOOOA0 62%	4340 I		HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.36	41	58
ORF2 [Rattus norvegicus] gi 56588 emb CAA37 50% 645.1 57% 57% 57% collagen type VII [Homo gi 495866 gb AAA58 58% 55% 965.1 64% 64% 64% 64% 65% 965.1 55% 965.1 55% 965.1 55% 965.1 55% 62% 62% 965.1 55% 9	4450 b	1P.	lastx.14	unknown protein [Homo sapiens]	gi 1196398 gb AAA8 8020.1	20%	254	177
collagen type VII [Homo gi 495866 gb AAA58 58% 55% 55% 965.1 47% 64% 57% 57% 57% 57% 57% 57% 57% 57% 57% 57	4483 b	þ	lastx.14	ORF2 [Rattus norvegicus]	gi 56588 emb CAA37	20%	168	293
collagen type VII [Homo gi 495866 gb AAA58 58% 55% 965.1 47% 64% 64% 575% 965.1 57% 62% 965.1 62% 965.1 62% 965.1					645.1	21%	280	342
collagen type VII [Homo gi 495866 gb AAA58 58% 55% 965.1 64% 64% 57% 57% 9FAM. PEAM.						57%	73	114
sapiens] 965.1 55% 47% 64% . 57% . 57% 33% 62% 62%	4630		blastx.14	collagen type VII [Homo	gi 495866 gb AAA58	28%	336	286
47% 64% 57% 57% 57% 62% 62% 62% 62% 62%				sapiens]	965.1	25%	93	40
64% 57% 32% 9FAM: DE00040						47%	155	105
57% 32% 33% 62%						64%	327	286
32% 33% 62% 62%					•	21%	799	225
33% 52% 62% 62%						32%	87	13
DE00040 62%	_					33%	81	ī
PFAM: PEONO40 6.75						62%	355	332
11 (1) (1) (1) (1) (1) (1) (1) (1) (1) (4662	1	HMMER	PFAM:	PF00049	6.75	286	318

	599	665	249	47	136	362		3	116		161	323	272	145	·		347		427			170	169	164	15	53
	348	270	416	193	258	237		104	151	;	262	406	310	113			228	,	395)		33	23	9	47	91
	47.92	%86	%86	71%	63%	8.41		94%	91%		38%	28%	53%	4.4			8.4		1.89)		20%	44%	41%	54%	46%
	PF00005	dbj BAA35501.1	gi 455170 gb AAA83	861.1		PF00119		gi 1790156 gb AAC7	6742.1	2144702041 1124 1	g1 4469304 emb CAA	25493.1		PF00271			PF00119		PF00130			gi 1196398 gb AAA8	8020.1		pir A27695 A27695	
Insulin/IGF/Relaxin family	PFAM: ABC transporters	Hypothetical protein HI0658 [Escherichia coli1	diaminopimelate	decarboxylase	Escherichia coli]	PFAM: ATP synthase A	chain	(AE000449) putative	xylanase [Escherichia coli]	n15E conformation	protection of the property of the protection of	sequence [Kirsten murine	sarcoma virus	PFAM: Helicases	conserved C-terminal	domain	PFAM: ATP synthase A	chain	PFAM: Phorbol esters /	diacylglycerol binding	domain	n protein [Homo	sapiens		synexin - bovine	(fragment)
1.8	HMMER 1.8	blastx.2	blastx.14			HMMER	1.8	blastx.14		blacty 14	OldolA.14			HMMER	1.8		HMMER	1.8	HIMMER	1.8		blastx.14		,	blastx.14	
	4666		4668			4715		4762		4790				4798			4823		4878		,	4910		1 1 0	4955	
	839088		954140		,	980908		888856	Ī	967668				724404			774280		506621		00.401.4	924211		0007	964882	
	HNGLG06		HNGLH82		10, 0, 0, 4,	HNGMM87		HNG0022		HNHAI11			0 7 12 12 12 12 12	HNHBEI9			HNHBY45		HNHDM74		02/1/11/11/11	HINHD Y50			HNHEJ85	

HNHET25 953410 HNHFA11 967126 HNHGD07 953416		5002	1.1 , 1.4			1000		
		3002	1.1 , 1.4			38%	91	53
			blastx.14	(AJ005562) SPR2D	gi 3093363 emb CAA	32%	347	246
	- 			protein [Mus musculus]	06591.1	43%	250	203
						46%	207	169
		5030	blastx.14	(AF144054) apoptosis	gi 4868437 gb AAD3	52%	212	355
				related protein APR-4	1316.1 AF144054_1	35%	342	401
		101	1-1	(A FOCOOT)				
		1716	blastx.14	(AF053091) eyelid	gi 2981221 gb AAC0	46%	164	241
				[Drosophila melanogaster]	6254.1	25%	227	280
						33%	295	384
to P Voca						30%	259	384
						20%	346	381
						36%	268	333
						76%	259	384
						62%	367	390
						42%	322	378
						62%	367	390
	1	\dashv				83%	367	384
		5127	blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	81%	2	112
HNHGH20 959499		5146	blastx.14	notch4 [Homo sapiens]	gi 1841543 gb AAC6	43%	56	6
					3097.1	77%	154	128
	1					33%	256	167
						33%	297	244
1	1					62%	131	108
HINHGV 22 0/4653		5189	HMMER	PFAM: Helicases	PF00271	4.66	94	138
			F.8	conserved C-terminal				
HNHHI10 964659		5251	blastx.14	ORF1 [Rattus norvegicus]	oi156587[emblCA A 37	7095	75	90
					644.1	34%	157	71

158	155	0+1	300	407	73	120	297	360	235		122	771		380			70		394	467	443	178	79	451
220	187	6	49	363	14	91	262	310	200		8	26		360))		2		77	408	393	83	47	365
33%	3.57		67.6	%09	45%	402	20%	47%	2.66			Υ:		4.12	!		22.31		100%	20%	47%	20%	54%	11.11
	PF00293		PF00607	gi 4680231 gb AAD2	7584.1 AF118275_1				PF00130		PF00442			PF00076			PF00130		gi 5106956 gb AAD3	9906.1 AF113615_1	1	gi 339771 gb AAA51	622.1	PF00169
	PFAM: Bacterial mutT	protein	PFAM: gag gene protein p24 (core nucleocapsid protein)	(AF118275) atrophin-	related protein ARP	[Homo sapiens]			PFAM: Phorbol esters/	diacylglycerol binding	PFAM: Ubiauitin	carboxyl-terminal	hydrolases family 2	PFAM: RNA recognition	motif. (aka RRM, RBD,	or RNP domain)	PFAM: Phorbol esters /	diacylglycerol binding domain	(AF113615) FH1/FH2	domain-containing protein	FHOS [Homo sapiens]	ORF2 contains a reverse	transcriptase domain.; ORF2 [Homo saniens]	PFAM: PH (pleckstrin
·	HMMER	1.8	HMMER 2.1.1	blastx.14					HMMER	N. 1.8	HMMER	1.8		HMMER	1.8		HMMER	8:	blastx.14			blastx.14		HMMER
	5266		5318	5496				1	5497		5512			5646			5682		9899			5702		5714
	765598		908419	934456				0000	955522		866951			471037			660053		68/0/6			954360	- 11	909971
	HNHHL74	a C TATAL CLA	HNHIA95	HNHPH29	4			TOTATO!	HOIAE91		HSATQ28			HSAYN79			HSYBL15		HSYDP04			HT3SA07		HT4GJ85

			1.8	homology) domain				
			blocty 14	(AE052074) CUIAD 70	122001 641 114 1 0 4			
			UlastA.14	(Ar 0339/4) 3 WAF-/0	g1 5290154 gb AAC4	23%	251	448
	·		-,	[Mus musculus]	0155.1	%88	4	54
						33%	448	492
HISEA69	952359	5721	blastx.14	(AL032624) cDNA EST	gi 3881086 emb CAA	37%	264	479
				yk321h8.5 comes from	21522.1	30%	123	251
				this gene; 1 from this gene	-			 }
				[Caenorhabditis elegans]		- Landar		
HTAAW46	719422	5735	HMMER	PFAM: HMG (high	PF00505	5.82	9	35
			1.8	mobility group) box			ı	3
HTABG87	940153	5745	HMMER	PFAM: Eukaryotic protein	PF00069	13.81	240	335
			1.8	kinase domain))
			blastx.14	(AF006064) protein	gi 2393890 gb AAC5	54%	8	139
				kinase homolog [Fowlpox	8236.1	33%	189	356
				virus])
HTACW17	961560	2160	blastx.14	(AC007660) unknown	gi 4895220 gb AAD3	37%	54	221
				protein [Arabidopsis	2806.1 AC007660_7	61%	212	265
				thaliana	l			
HTAFE69	944409	2797	blastx.2	(AK000496) unnamed	dbj BAA91205.1	%69	432	704
				protein product [Homo				
1177 4 111 4 7	0,000	1		Sapielis				
HIAHL45	908949	5817	HMMER 2.1.1	PFAM: SCAN domain	PF02023	228.7	268	555
			blastx.14	(AC004522) Zn-finger-	gi 3006231 gb AAC0	65%	220	534
				like protein; similar to	9486.1	36%	529	642
				Z98745 (PID:g2924250)	-	•	ì	1
				[Homo sapiens]				
HIAHV04	926747	5826	blastx.14	(AC005757) R32611_1	gi 3688089 gb AAC6	100%	3	446
TTT A TOO	1 2 0 0 0 0			[Homo sapiens]	2258.1			
HIAJN08	958057	5841	HMMER	PFAM: Helicases	PF00271	5.49	20	55
							,	, ,

gl 486843/ gb AAD3 1316.1 AF144054_1 PF00620
PFAM: RhoGAP domain PF00620
predicted protein shows 1 86318.1
Counces from this gene;
EMBL:D32994 comes
gi 1185397 gb AAA8
7791.1
,
PF00588
alternate gene name yibK gi 466744 gb AAB18
583.1
PF01784
(AL034490) similar to gil4008560lemblCAA
yeast ngg1-interacting 22481.1

414	1065	433	305	305	27	203	110	275	443	209	325	160	1190
361	970	398	27	320	-	174	21	3	3	162	242	2	1020
61%	28%	7.26	191	95%	%88	2.4	30.7	76%	87%	3	35.64	58%	32.41
		PF00130	PF00883	gi 1054725 emb CAA 60164.1		PF00018	PF00562	gi 2739048 gb AAB9 - 4600.1	gi 1787452 gb AAC7 4286.1	PF00099	PF00023	gi 5923874 gb AAD5 6394.1 AF182426_1	PF00069
Schizosaccharomyces	[bombe]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Cytosol aminopeptidase family	aminopeptidase A [Escherichia coli]		PFAM: Src homology domain 3	PFAM: RNA polymerase beta subunit	(AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]	(AE000218) putative adhesion and penetration protein [Escherichia coli]	PFAM: Zinc-binding metalloprotease domain	PFAM: Ank repeat	(AF182426) arylacetamide deacetylase [Rattus norvegicus]	PFAM: Eukaryotic protein
		HMMER 1.8	HMMER 2.1.1	blastx.14		HMMER 1.8	HMMER 2.1.1	blastx.14	blastx.14	HMMER 1.8	HMMER 1.8	blastx.14	HMMER
	·	5936	5944			5949	2968		5973	9665	9601	9509	6081
		685425	967047			683469	923443	•	974590	602099	880424	948518	008996
		HTGEL46	HTGEQ11			HIGER/2	HTGFZ03		HTGGL23	HTHCB68	HTJAB35	HTJMT23	HTOAK34

			1.8	kinase domain				
			1.1	A TOO 400 EX				
			olastx.14	(AF084205)	gi 3452473 gb AAC7	75%	954	1190
				serine/threonine protein	1014.1			
				kinase TAO1 [Rattus				
				norvegicus				
HTODG16	909952	6108	HMMER 2.1.1	PFAM: RasGEF domain	PF00617	148.5	4	402
			blastx.14	CDC25 [Saccharomyces kluyveri]	gi 171187 gb AAA34 479.1	34%	13	399
HTOFT34	527144	6146	HMMER	PFAM: Phorbol esters/	PF00130	4.53	235	264
			». 	diacylglycerol binding domain				
HTOHL35	537364	6173	HMMER	PFAM: Zinc finger, C2H2	PF00096	6.52	4	33
COLLEGE			1.8	type	!		•)
HIOIY09	836003	6201	HMMER	PFAM:	PF00049	7.08	19	123
			1.8	Insulin/IGF/Relaxin family			•	3
HTSHF47	720403	6229	HMMER	PFAM: Helix-loop-helix	PF00010	7.82	105	140
OCA MITOTIL	0,000		1.0	DINA-binding domain				
H1SHM38	972248	6230	HMMER 2.1.1	PFAM: EGF-like domain	PF00008	72	299	406
			blastx.14	(AB011532) MEGF6	gi 3449294 dbj BAA3	%88	287	538
				[Rattus norvegicus]	2462.1	20%	278	460
						53%	320	466
	•					42%	299	460
						42%	287	442
						43%	290	427
			-			40%	341	481
						46%	287	415
						<u>}</u>	114	173
						%99	413	457

50% 467 538 35% 245 283 47% 472 284 284 50% 245 295 246 245 50% 245 283 284 283 50% 245 283 284 283 60% 245 283 284 283 80% 482 283 284 283 80% 482 535 284 283 80% 482 535 284 283 80% 482 535 284 281 80% 434 532 284 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80% 434 532 80%
50% 61% 61% 83% 83% 847% 85% 80% 80% 80% 80% 80% 80% 80% 80% 80% 80

286	460	232	505	376	280	445	268	532	343	262	283	406	505	532	406	379	280	483	268	544	382	376	382	223	235	262	406	409	376	379
230	401	203	473	308	245	329	245	485	251	227	251	296	485	473	344	359	245	454	245	491	320	344	359	203	203	215	359	356	320	320
36%	40%	%09	54%	34%	20%	25%	62%	37%	73%	20%	45%	24%	71%	40%	33%	71%	20%	%09	62%	33%	33%	63%	62%	71%	45%	37%	37%	38%	36%	40%
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280	306	434	219	217	241	48	70	777	330	137	176	370	450	547 479	123	299
251	220	613	172	104	47	16	20	869	61	72	144	230	367	373	76	3
%09	15.45	88%	4.95	23.9	78%	45%	41%	54%	123.2	92.9	2.21	%16	——————————————————————————————————————	52%	2.87	50.1
	PF00125	gi 3800742 gb AAC6 8839.1	PF00271	PF00171	gi 2766693 gb AAB9	5478.1		gi 5360271 dbj BAA8	PF01425	PF00505	PF00130	gi 206535 gb AAA41	994.1		PF00293	PF01432
	PFAM: Core histones H2A, H2B, H3 and H4	(AF036548) RGC-32 [Rattus norvegicus]	PFAM: Helicases conserved C-terminal	domain PFAM: Aldehyde dehydrogenase family	(AF038838) proline	dehydrogenase [Klebsiella	aerogenes	(AB029335) HrPET-3 [Halocvnthia roretzi]	PFAM: Amidase	PFAM: HMG (high mobility group) box	PFAM: Phorbol esters / diacylglycerol binding	RAB14 [Rattus	norvegicus]		PFAM: Bacterial mutT protein	PFAM: Peptidase family M3
	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 2.1.1	blastx.14			blastx.14	HMMER 2.1.1	HMMER 1.8	HMMER 1.8	blastx.14			HMMER 1.8	HMMER 2.1.1
	6260	6539	6314	6359				9989	9367	6394	6403	6420			6425	6453
	869547	918641	812705	924996				885996	784768	869397	529745	912611			783572	947789
	HTWCG65	HTWEY30	HTWJA59	HTXCY84				HTXDW14	HTXDX61	HTXFN69	HTXGL73	HTXJ168			HTXJM73	HTXKQ55

blastx.14 mitochondrial intermediate nentidase
_
6525 blastx.14
6555 HMMER 2.1.1
6560 blastx.14
_
6575 HMMER 2.1.1
blacty 14
(EC 5.99.1) [Escherichia
6577 blastx.14 (AF077042) 30S
ribosomal protein S7
6579 blastx.2 (AB016962) synGAP-b1
6586 blastx.14 (AF051325) SH3 domain
6589 blastx.14
reverse transcriptase [Homo sapiens]
6597 blastx.14 (AF151854) CGI-96

278	212	373	376	433	509	969	313	367	367	354	1035
06	09	332	344	251 766	859	3	251	200	200	118	868
65.3	54%	2.21	3.68	39%	104.26	100%	6.01	79.5	%96	46%	25.8
PF01352	gi 2789430 dbj BAA2 4380.1	PF00130	PF00293	gi 3947651 emb CAA 22138.1	PF00059	gb AAF37804.1 AF1 75206_1	PF00096	PF01433	gb AAF07395.1 AF1 06037_1	gj 213868 gb AAA49 614.1	PF01437
PFAM: KRAB box	repressor protein [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Bacterial mutT protein	(AL033536) predicted using Genefinder; similar to 1 1 1 elegans!	PFAM: Lectin C-type domain short and long forms	(AF175206) lectin-like receptor F1 [Homo sapiens]	PFAM: Zinc finger, C2H2 type	PFAM: Peptidase family M1	(AF106037) adipocytederived leucine aminopeptidase [Homo sapiens]	Zn-binding protein [Pleurodeles walt]	PFAM: Plexin repeat
HMMER 2.1.1	blastx.14	HMMER 1.8	HMMER 1.8	blastx.14	HMMER 1.8	blastx.2	HMMER 1.8	HMMER 2.1.1	blastx.2	blastx.14	HMMER 2.1.1
6612		6619	2699		9599		6691	<i>L</i> 699		8699	6710
908541		923734	943074		957347		868490	947915	,	907631	888685
HWAAF66		HWAAY03	HWACA38		HWADF26		HWAEN20	HWAFW39		HWAFX39	HWAGM33

T	_			П					Π.			Т		т-			т-		_								т			
283	639	471	396	583	343	412	1198	1798	484	510		424	!	868)		205) 	766	1040	863	336		434	306	270	156	7	69	118
215	535	409	295	1215	513	642	1272	1824	278	487		531	 	857			185		806	066	837	184		273	217	172	203	84	125	150
47%	34%	42%	29%	62%	%99	45%	44%	%99	63%	75%		100%		4.8			4.15		83%	100%	%88	38.64		81%	%96	36%	62%	34%	36%	63%
gi 1196433 gb AAA8	8038.1			gi 709961 gb AAC52	167.1				gi 5020264 gb AAD3	8043.1 AF151363_1		gi 4929707 gb AAD3	4114.1 AF151877 1	PF00076			PF00099		gi 5441611 emb CAB	46854.1		PF00010		gi 4689256 gb AAD2	7831.1[AF121858_1		gi 334072 gb AAA47	471.1		
unknown protein [Homo	sapiens			retinoid X receptor	interacting protein [Mus	musculus]			(AF151363) Cdc42	GTPase-activating protein	[Mus musculus]	(AF151877) CGI-119	protein [Homo sapiens]	PFAM: RNA recognition	motif. (aka RRM, RBD,	or RNP domain)	PFAM: Zinc-binding	metalloprotease domain	(AJ388555) hypothetical	protein [Canis familiaris]	۸	PFAM: Helix-loop-helix	DINA-binding domain	(AF121858) sorting nexin	8 [Homo sapiens]		ORF-3 protein	[Pseudorabies virus]		
blastx.14				blastx.14					blastx.14			blastx.14		HMMER	1.8		HMMER	1.8	blastx.14			HMMER 1	1.8	blastx.14			blastx.14			
6711				6714	-				6715	-		6720		6722			6741		6771			6785		6820			6831			
985656			,	960646		-	·	1,7,000	299606			959449		868363	_		747723		963498			682583		915050			926017			,
HWAGX37			0 7444 7 74444	HWAHII0				100011111111	HWAHS94			HWBAL44		HWBAQ16			HWBBR65		HWBDM24		T 02 % CA CA AAA A	HWBEXZ/	00011	HYAAF33			HYAAS08			

211	427	27	36	112	591	688	597	420	684	142	654	388	562	<u> </u>		464		17	142	264	300
282	257	206	263	2	505	869	382	103	604	2	619	263	2			141		112	195	398	365
37%	27.8	6'06	67%	47	33.3	71%	26%	46%	10%	48%	%99	32.5	92%			34%		34%	20%	28%	40%
	PF00047	PF00207	gb AAA39508.1	PF00617	PF00036	gi 4038292 gb AAC9	7349.1					PF00643	gi 4325109 gb AAD1 7259.1	•		emb[CAA97423.1]		gi 5305335 gb AAD4	1594.1 AF071081_1		
	PFAM: Immunoglobulin domain	PFAM: Alpha-2- macroglobulin family	alpha-2-macroglobulin [Mus musculus]	PFAM: RasGEF domain	PFAM: EF hand	(AF106071) ras activator	RasGRP [Homo sapiens]					PFAM: B-box zinc finger.	(AF119043) transcriptional	intermediary factor 1	gamma; TIF1gamma [Homo sapiens]	predicted using	Generinaer [Caenorhabditis elegans]	(AF071081) proline-rich	mucin homolog	[Mycobacterium	tuberculosis
	HMMER 2.1.1	HMMER 2.1.1	blastx.2	HMMER 2.1.1	HMMER 2.1.1	blastx.14						HMMER 2.1.1	blastx.14			blastx.2		blastx.14			
	6848	0989		6863	6883							2689				6918		6934			
	971448	900008		956606	862606							909031				944080		509696			
	HYABP53	HYABB43		HYAAU65	HWBEG18							HWBCS08				HWBAQ71		HWAFG12			

) 142	101	300	5 297		306			3 14	3 14		13		_	165			328		273	162				372	475		493	
219				332	338	365	314	208	178	253	78	93	249	221	240	237	357	248	40	7	169	400	346	316	116		98	477
34%	44%	32%	34%	34%	93%	75%	38%	29%	20%	40%	77%	52%	%92	42%	75%	42%	%06	25%	23.2	55%	29%	%09	38%	42%	147.95		%86	%08
		e ²	~~~~					gb AAC08737.1						•					PF00047	emb CAA46948.1					PF00071		gb AAA42000.1	
		MANAGE AND THE STATE OF THE STA	no de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	•				(AF010144) neuronal	thread protein AD7c-NTP	[Homo sapiens]					-		-		PFAM: Immunoglobulin domain	CMRF-35 antigen [Homo	sapiens]				PFAM: Ras family	binding P-loop)	rab-related GTP-binding	protein [Rattus
								blastx.2											HMMER 2.1.1	blastx					HIMIMER	0.1	blastx.2	
								6938											6942						6946			
				·-				948858											887166						931547			
							į	HWAFA47											HWAEU35						HWAEG71		- 147 - P	

	3 215	12 209				280 552	_			67 381																	
	29.5	%69	%02	31%	29%	96			225.7	225.7	225.7	225.7	225.7 91% 82% 100%	225.7 91% 82% 100% 77%	225.7 91% 82% 100% 77% 100%	225.7 91% 82% 100% 77% 100%	225.7 91% 82% 100% 77% 100% 89%	225.7 91% 82% 100% 77% 100% 89% 89%	225.7 91% 100% 77% 100% 89% 89% 71% 58%	225.7 91% 82% 100% 77% 100% 89% 71% 58% 87%	225.7 91% 100% 100% 100% 89% 89% 71% 58% 87% 100%	225.7 91% 100% 77% 100% 89% 71% 58% 87% 100% 54%	225.7 91% 82% 100% 77% 100% 89% 71% 58% 87% 100% 54% 60%	225.7 82% 100% 100% 99% 89% 71% 58% 87% 100% 54% 60% 81%	225.7 91% 100% 77% 100% 89% 71% 58% 87% 100% 54% 60% 81%	225.7 82% 100% 100% 99% 89% 71% 58% 87% 100% 54% 60% 81% 83%	225.7 82% 100% 77% 100% 89% 87% 100% 54% 60% 81% 83% 40%
	PF00435	gi 5262574 emb CAB	45729.1			PF01163		00,100	PF01182	PF01182	PF01182 emb CAA03416.1	PF01182 emb CAA03416.1 gi 4826478 emb CAB	PF01182 emb CAA03416.1 gi 4826478 emb CAB 42896.1	PF01182 emb CAA03416.1 gi 4826478 emb CAB 42896.1	PF01182 emb CAA03416.1 gi 4826478 emb CAB 42896.1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1	emb CAA03416.1 gi 4826478 emb CAB 42896.1 gi 4959568 gb AAD3 4394.1 AF132984_1
norvegicus]	PFAM: Spectrin repeat	(AL080133) hypothetical	protein [Homo sapiens]			PFAM:	RIO1/ZK632.3/MJ0444 family	PFAM: Glucosamine-6-	O OTTITUTO ONTO THE T	phosphate isomerase	phosphate isomerase unnamed protein product [unidentified]						duct ng ns]	te isomerase I protein product iffed] o SH3-binding Homo sapiens] Romo la pore interacting NPIP [Homo	duct ng ns] pore	te isomerase I protein product ified] o SH3-binding Homo sapiens] 84) nuclear pore interacting APIP [Homo	te isomerase I protein product iffed] o SH3-binding Homo sapiens] 84) nuclear pore interacting APIP [Homo	te isomerase I protein product ified] o SH3-binding Homo sapiens] 84) nuclear pore interacting APIP [Homo	te isomerase I protein product ified] o SH3-binding Homo sapiens] N84) nuclear pore interacting APIP [Homo	te isomerase I protein product ified] o SH3-binding Homo sapiens] 184) nuclear pore interacting APIP [Homo	te isomerase I protein product ified] o SH3-binding Homo sapiens] New Paper pore interacting APIP [Homo	te isomerase I protein product iffed] o SH3-binding Homo sapiens] New Sapiens SHOM SA Nuclear pore interacting APIP [Homo	te isomerase I protein product ified] o SH3-binding Homo sapiens] Why nuclear pore interacting APIP [Homo
	HMMER 1	 				HMMER I					2.1.1 p																
	6947					9569		6971	1	1	,	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984	6984
	958115	·				756888		949088				944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903	944903
	HWAEC08					HWACY70		HWABG11				HUUDR34	HUUDR34	HUUDR34	HUUDR34	HUUDR34 HUUCJ02	HUUCJ02	HUUDR34	HUUDR34	HUUDR34	HUUDR34	HUUDR34	HUUDR34 HUUCJ02	HUUDR34	HUUCJ02	HUUDR34 HUUCJ02	HUUDR34

						%99	300	274
HTX0015	869261	7011	HMMER 2.1.1	PFAM: Ubiquitin family	PF00240	44.9	130	273
HTXLS08	958357	7023	blastx.14	(AF090989) high-risk	gi 4151328 gb AAD1	48%	745	786
				human papilloma viruses	2543.1	%89	1006	1146
				E6 1 alpha [Homo		41%		237
				sapiens]		21%	511	645
						10%	427	477
						27%	580	645
HIWKB07	952841	7085	blastx.14	(AF003535) ORF2-like	gi 2197085 gb AAD0	%09	. 25	84
				protein [Homo sapiens]	4635.1	75%	259	294
						20%	205	258
						33%	36	116
				ī		%02	167	196
HTWJH08	790185	7087	blastx.2	(AK000385) unnamed	dbj BAA91131.1	61%	197	51
				protein product [Homo sapiens]				
HTWJH08	846554	9615	blastx.2	(AK000385) unnamed	dbj BAA91131.1	61%	197	51
				protein product [Homo sapiens]				
HTWJF50	911448	6802	blastx.14	myosin I [Rattus	gi 3724141 emb CAA	48%	1009	1428
				norvegicus]	50871.1	53%	334	681
						25%	732	851
						46%	863	1012
						39%	40	108
O FOLLANDATI	, 0,70					20%	989	715
німғQі9	586124	7091	HMMER 2.1.1	PFAM: Sema domain	PF01403	62.9	14	184
HTOIA82	844319	7198	HMMER	PFAM: Zinc-binding	PF00099	4.25	50	82
HTOHI14	659280	7204	HMMER	PFAM: Acnaraginace	DE01112	1000	1 40	5
			NATIONAL PROPERTY.	11 Crivi. Asparaginase	1101112	7.07	140	/17

	367	183	096	1017	216	394	397	293 392	386	359	275	510	59
	5	162	580	601		320	281	6 297	478	823	225	406	500
	33%	52% 45%	105.2	65%	%08	29.5	64%	48%	25.9	%68	%92	48%	47% 44%
	gi 5814097 gb AAD5 2099.1 AF106069_1	dbj BAA91951.1	PF00856	gi 4153862 gb AAD0 4721.1	gi 2150044 gb AAB5 8795.1	PF00621	gi 3876654 emb CAA 18349.1	gi 3170887 gb AAC4 0165.1	PF00397	gi 603953 dbj BAA07 893.1	gi 2065210 emb CAA	73251.1	
	(AF106069) deubiquitinating enzyme [Homo sapiens]	(AK001868) unnamed protein product [Homo sapiens]	PFAM: SET domain	(AC005065) determined by GENSCAN prediction and 1	(AF001293) aiolos [Mus musculus]	PFAM: RhoGEF domain	(AL022271) similar to Guanine nucleotide exchange 1 1 1 this g	(AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus]	PFAM: WW domain	This gene is novel. [Homo sapiens]	Pro-Pol-dUTPase	polyprotein [Mus	ınuscunusj
2.1.1	blastx.14	blastx.2	HMMER 2.1.1	blastx.14	blastx.14	HMMER 2.1.1	blastx.14	blastx.14	HMMER 2.1.1	blastx.14	blastx.14		
	7222	7282	7305		7311	7364		7365	7369		7370	•	
	960113	946168	963862		909806	910040		965738	959129	:	932459		
	НТОРМ08	HTHBY73	HTGEX10		HTGEA37	HTAIF22		HTAIF11	HTAEV23		HTAEP05		

						77%	386	412
HTABK47	720684	7379	HIMIMER 2.1.1	PFAM: Monooxygenase	PF01360	23.3	371	430
HSYCV01	940661	7408	HMMER	PFAM:	PF00369	7.29	448	492
			1.8	Hydroxymethylglutaryl-				
HSAWR08	959943	7458	blastx.14	(AL110271) hypothetical	gi 5817084 emb CAB	%86	123	287
				protein [Homo sapiens]	53709.1	!		
HSAUL84	908440	7504	HIMMER	PFAM: gag gene protein	PF00607	43.3	105	302
			2.1.1	pz4 (core nucleocapsia protein)				
			blastx.14	gag protein [Human	gi 1780975 emb CAA	83%	. 135	299
				endogenous retrovirus K]	71418.1	%09	24	152
HNHOF94	948720	7551	blastx.2	(AK000496) unnamed	dbj BAA91205.1	%19	176	484
				protein product [Homo saniens]				
HNHNP81	928378	7554	HMMER	PFAM: 7 transmembrane	PF00001	58.09	233	511
			1.8	receptor (rhodopsin family)				
			blastx.2	(AF091575) olfactory	gb AAC64595.1	61%	236	505
				receptor [Rattus norvegicus]		52%	505	618
HNHLC01	915363	7581	blastx.14	unknown protein [Homo	gi 1196431 gb AAA8	46%	5	82
				sapiens]	8036.1	40%	57	131
						36%	133	207
						61%	219	257
						46%	260	304
HNHGV62	743400	7603	blastx.2	(AK000385) unnamed	dbj BAA91131.1	62%	52	285
				protein product [Homo sapiens]		%91	287	349

HNHGE31	698046	7624	HMMER	PFAM: Zinc-binding	PF00099	3.3	83	109
			1.8	metalloprotease domain				
HNHFV49	975415	7644	blastx.2	hypothetical protein (L1H	pir B34087 B34087	81%	483	190
				3' region) - human		71%	227	9
						%06	217	188
HNHFH24	903741	7657	HMMER	PFAM:	PF00209	37.2	208	306
			2.1.1	Sodium:neurotransmitter				
				symporter family				
			blastx.14	(AF075266) orphan	gi 3347930 gb AAC2	%9L	187	327
				transporter isoform B9	7761.1	27%	414	467
				[Mus musculus]				•
HNHDF07	953883	7702	HMMER	PFAM: Fibronectin type	PF00041	7.48	242	319
			1.8	III domain				
HNHDC29	904546	7704	blastx.14	contactin associated	gi 1857708 gb AAB4	%86	219	7
				protein [Homo sapiens]	8481.1			
HNHCI32	861673	7716	HMMER	PFAM: 7 transmembrane	PF00001	133.17	195	545
			1.8	receptor (rhodopsin				
				family)			_,	
			blastx.2	(AF112461) G protein-	gb AAF27279.1 AF1	100%	189	551
				coupled receptor 57	12461_1	100%	112	186
				[Homo sapiens]	,	100%	99	112
HNHCI32	956105	9645	HMMER	PFAM: 7 transmembrane	PF00001	133.17	951	601
***************************************			1.8	receptor (rhodopsin				
				family)				
			blastx.2	(AF112461) G protein-	gb AAF27279.1 AF1	100%	555	917
				coupled receptor 57	12461_1	100%	478	552
				[Homo sapiens]		100%	422	478
HNHBF47	949027	7731	HMMER	PFAM: Cadherin	PF00028	44.76	899	522
			1.8					
			blastx.2	(AB028499) Flamingo 1	dbj BAA84070.1	%96	409	999
							1	

259	923	398	099	099	099	968	669	884	890	247	253	648	235	884	247	247	878	669	854	708	380	380	398	371	371	362	829	262	764	374
5	999	243	412	370	412	699	355	999	648	20	Ť	361	14	654	14	26	999	412	672	433	270	270	270	270	270	264	683	2	723	270
92%	91%	%98	42%	36%	36%	43%	33%	43%	39%	38%	32%	30%	36%	39%	37%	35%	35%	32%	37%	28%	40%	35%	37%	44%	38%	33%	32%	73%	57%	35%
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llus]																								,						
[Mus musculus]																														
																			·								-			
		_												_							-									

2 480		1 677	3 364	989 /	1 84		5 1071				·····									477	9 440	490		143
412	330	81	173	87		10					724								499	299	366	464		340
39%	46.67	75%	84%	33%	93%	40%	%86	40%	42%	32%	37%	100%	77%	30%	%68	35%	40%	36%	20%	78%	4.43	2.07		62%
	PF00028	gb AAD43734.1 AF1	52473_1				gi 5456892 gb AAD4	3697.1												gi 5360091 gb AAD4 2864.1 AF155098 1	PF00175	PF00130		gb AAC08737.1
	PFAM: Cadherin	(AF152473)	protocadherin alpha C1	short form protein [Homo	sapiens]		(AF152303)	protocadherin alpha Cl	[Homo sapiens]						-	,				(AF155098) NY-REN-8 antigen [Homo sapiens]	PFAM: FAD/NAD-binding domain in oxidoreductases	PFAM: Phorbol esters /	diacylglycerol binding domain	(AF010144) neuronal
	HMMER 1.8	blastx.2					blastx.14													blastx.14	HMMER 1.8	HMMER	1.8	blastx.2
	7745						9649													7757	6922	7778		7781
	742116						955094													969158	918626	915294		950173
	HNHAF61						HNHAF61				-									HNG0Z40	HNGNY02	HNGND01		HNGMW65

247	247	3	25	111	346	152	351	125	18	349	392			77	2	42	210	526	817	2	2	2	7	2	7	2	<u></u>
417	345	80	81	200	414	205	392	202	98	269	219			199	43	11	242	437	2	196	193	199	196	193	199	193	196
45%	%09	25%	%89	43%	43%	55%	64%	21%	47%	6.93	%6L			41%	71%	83%	72%	5.95	40%	61%	62%	54%	52%	54%	53%	20%	44%
										PF00031	gi 4186073 emb CAA	09423.1		sp Q29386 Q29386				PF00505	emb CAB55945.1	gi 506502 emb CAA5	6225.1						
[Homo sapiens]			-							PFAM: Cystatin domain	(AJ010949) calcium	channel alpha-2-delta-C	subunit [Mus musculus]	KERATIN TYPE II	CYTOSKELETAL 8	(FRAGMENT).		PFAM: HMG (high mobility group) hox	(AL117470) hypothetical protein [Homo sapiens]	NK10 [Mus musculus]							
							-			HMMER 1.8	blastx.14			blastx.14				HMMER 1.8	blastx.2	blastx.14							
	-		-							7788	7791			7795				7801		7837							
			~							974358	948825			952236				942758		964715							
	*									HNGMD48	HINGLY08			HNGLL07				HNGKM74		HNGIR10							

2	92	83	=	2	2	104	197	256	238	130	921	466		206	200	520	283	214	317	152	368	292	205	104	82	284	320	19
193	199	196	178	217	115	181	232	309	306	285	986	290		700	/07	404	230	140	258	39	324	381	276	154	210	261	391	93
45%	61%	57%	37%	76%	39%	46%	20%	33%	30%	78%	%98	33.71		240/	0/+/0	41%	77%	36%	%02	42%	53%	36%	20%	47%	20%	5.01	45%	40%
										gi 4186073 emb CAA	.09423.1	PF00047		αh A D 3 4 0 4 Ε 1 1 A Ε 1	golfxx.03+3+0.1[fx1.1]	43185_1			gi 509838 gb AAA87	332.1		gi 439877 gb AAB02	291.1			PF00098	gi 2072966 gb AAC5	1272.1
										(AJ010949) calcium	channel alpha-2-delta-C subunit [Mus musculus]	PFAM: IG	(immunoglobulin)	(AF143185) high affinity	(11111) ingili ailiili)	ımmunoglobulin gamma	Fc 1		pol polyprotein [Baboon	endogenous virus]		reverse transcriptase	[Homo sapiens]			PFAM: Zinc finger, CCHC class	p40 [Homo sapiens]	
				_						blastx.14		HMMER	1.8	hlaetx	Cidolor				blastx.14			blastx.14				HMMER 1.8	blastx.14	
										1879		7897							7902			7933				7952	7973	
										941480		951489							967314	-		967512				959964	959977	
								· -		HNGFF50	:	HNGEO79							HNGEI11			HNGDM11				HNGDA08	HNGAZ08	

100	792	115	150	64	91	91	91	232	44	316	340	125	307	6	113	}	200	518	909	594	403	131	244
144	316	14	200	384	387	420	339	387	79	402	360	18	68	68	51	3	24	3	550	550	281	48	134
40%	35%	100%	2.96	%06	44%	42%	38%	44%	100%	27%	85%	40.5	84%	100%	27.49		32.11	78%	63%	53%	36%	46%	35%
		gi 4680667 gb AAD2 7723.1 AF132948_1	PF00047	gi 3894323 dbj BAA3	4639.1					-		PF00797	gi 2624972 gb AAB9	4880.1	PF00335		PF00240	gi 5733824 gb AAD4	9751.1 AF176069_1		gi[53669 emb CAA37	876.1	
		(AF132948) CGI-14 protein [Homo sapiens]	PFAM: IG (immunoglobulin) superfamily	(AB020063) Keap1 [Mus	musculus]		•					PFAM: N- acetyltransferase	(AF020313) proline-rich	protein 48 [Mus	PFAM: 4 transmembrane	segments integral	PFAM: Ubiquitin family	(AF176069) ubiquilin	[Homo sapiens]		decorin (PGII) [Mus	musculus]	
		blastx.14	HMMER 1.8	blastx.14								HMMER 2.1.1	blastx.14		HMMER	1.8	HMMER 1.8	blastx.14			blastx.14		
		7997	8003	8051								2908	8125		8141	i i	8184				8196		
		966347	733297	955894								529571	909931		893995	• •	927097				921263		
		HNFID11	HNFHR56	HNEDO77								HNEBJ81	HMWEN61		HMWBT59		HMSMN71				HMSJL53	,	

HMSHE81	784966	8218	HMMER 2.1.1	PFAM: PX domain	PF00787	29.1	128	421
HMSDL70	266606	8240	blastx.14	(AF083331) kinesin-like protein KIF1B [Rattus norvegicus]	gi 3493139 gb AAC3 3292.1	100%	2	103
HMSB095	796724	8258	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.61	273	302
HMMBL55	731523	8320	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.03	227	271
HMMAT08	500656	8327	blastx.14	DOCK180 protein [Homo sapiens]	gi 1339910 dbj BAA0 9454.1	49%	137	301
HMCHZ77	771795	8350	HMMER 2.1.1	PFAM: Nucleoside transporter	PF01733	81.6	5	283
HMALZ77	856266	8362	HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	88.5	2	232
HMAJL09	950168	8365	HMMER 1.8	PFAM: ADP-glucose pyrophosphorylase	PF00483	150.92	20	256
·			blastx.14	f270 [Escherichia coli]	gi 290545 gb AAA62 048.1	100%	254	469
HMAIQ20	669436	8367	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	3.43	172	234
HMAIH15	956705	8368	blastx.2	Hypothetical protein MJ0456 [Escherichia coli]	dbj BAA35499.1	100%	3	203
HMAIA55	899404	8369	blastx.2	(AF027204) putative tetraspan transmembrane protein L6H [Homo sapiens]	gb AAB82947.1	35%	188	532
HMADF74	944465	8377	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	42.8	369	440

674	176	365	420	989	131	608	487	519	134	-	_	408			1326	151	+C /	252	 }		252	365	100	504
294	418	222	133	486	33	723	398	436	96)		304			1249	710	/ 10	157	•		157	333	41	160
34%	116	59.8	%88	95%	%96	82%	%06	13.18	4.45	!		22.8			12.84	3 14	t T	40.5		-	%59	72%	30%	101.9
emb CAA76000.1	PF01263	PF02096	gi[53169 emb CAA36	803.1				PF00125	PF00076			PF00701			PF00125	PEUUOO		PF00147			gi 4378598 gb AAD1	9608.1		PF00651
leucine-rich repeat protein	PFAM: Aldose 1- epimerase	PFAM: 60Kd inner membrane protein	GTP binding protein [Mus	musculus				PFAM: Core histones H2A, H2B, H3 and H4	PFAM: RNA recognition	motif. (aka RRM, RBD,	or RNP domain)	PFAM:	Dihydrodipicolinate	synthetase family	PFAM: Core histones	PFAM: Zinc-binding	metalloprotease domain	PFAM: Fibrinogen beta	and gamma chains, C-	terminal globular domain	(AF107253) angiopoietin	Y1 [Homo sapiens]		PFAM: BTB/POZ domain
blastx.2	HMMER 2.1.1	HMMER 2.1.1	blastx.14					HMMER 1.8	HMMER	1.8		HMMER	2.1.1		HMMER 18	HMMER	1.8	HMMER	2.1.1		blastx.14			HMMER
	8379	8381	8386					8387	8401			8431			8459	8463		8555					}	8581
	922354	388074	932994	4	-		,	703776	966539			943886			949401	790234		910804						887375
	HMACV54	HMABD66	HLYHK61					HLYHK34	HLYGQ11			HLYEA70			HLYCF37	HLYBX91		HLMHL66					10 10 111	HLCDA67

	146	212	206	200	206	206	212	233	212	191	212	206	191	212	212	149	149	161	212	149	234	234	234	234	234	234	234	234	234
	78	3	m	3	3	9	6	n	18	3	21	3	21	3	12	33	3	9	69	3	166	172	172	172	181	181	181	154	181
	39.9	62%	64%	26%	54%	26%	47%	45%	43%	49%	40%	38%	43%	40%	43%	42%	42%	48%	37%	36%	39%	47%	38%	33%	44%	20%	55%	25%	20%
	PF00096	gb AAB97932.1																											
	PFAM: Zinc finger, C2H2 type	(AC004076) R30217_1	[Homo sapiens]				- Art Proper				an an an																		
2.1.1	HMMER 2.1.1	blastx.2																		***************************************							 		
	0098																												
	909242																												
	HJPAY56											. <u>.</u>								_									

8743 blastx.14 The hal 438 gene product is related to a C728
protein 1
8761 HMMER PFAM: Helicases
1.8 conserved C-terminal domain
8765 HMMER PFAM: FAD binding 2.1.1 domain
blastx.2 Aip2p [Saccharomyces
cerevisiae
IMER
blastx.2 (AF117210) host cell
factor 2 [Homo sapiens]
8771 HMMER PFAM: Core histones 1.8 H2A, H2B, H3 and H4
[Homo sapiens]
4.74

						34%	328	468
						61%	241	279
						35%	328	411
						41%	337	408
						41%	241	267
	-					63%	241	273
						28%	244	279
						%99	306	332
						35%	185	244
						28%	394	468
\mid HDTJF05	931977	8804	blastx.14	polyprotein [Hepatitis C	gi 464178 dbj BAA03	%85	394	438
				virus]	581.1	47%	168	218
						20%	49	96
						%09	208	237
						75%	258	281
HDTI074	933606	8805	blastx.14	(AL021749) protein	gi 2842482 emb CAA	45%	148	5
				phosphatase 2C-like	16879.1			
				protein [Arabidopsis				
				thaliana]				
HDTI016	934151	9088	HIMMER	PFAM: WD domain, G-	PF00400	117.6	164	283
			2.1.1	beta repeat				
			blastx.14	(AF072880) SOCS box-	gi 4754060 gb AAD2	%66	2	613
				containing WD protein	8808.1 AF072880_1	85%	610	672
				SWiP-1 [Homo sapiens]		%02	989	715
HDTDP02	919572	8831	blastx.14	(AF151872) CGI-114	gi 4929697 gb AAD3	%9L	135	212
				protein [Homo sapiens]	4109.1 AF151872_1			
HDTDD72	587710	8836	HMMER	PFAM: ATP synthase A	PF00119	85.33	165	350
			1.8	chain				
HDTDB37	669285	8844	HMIMER	PFAM: Zinc-binding	PF00099	2.43	201	218
•			1.8	metalloprotease domain		•		
HDTCC55	934923	8846	blastx.14	(AL117483) hypothetical	gi 5911963 emb CAB	46%	306	389
						2		200

453 542	4 105	105 167	615 1004	278 667	1331 1408	1331 1408		99 146	- 1 1	1783 1067	1723 1070	67 135	1 252	144 410	192 263			335 553	
46%	35%	42%	53.09	53.23	12.8	12.8		4.29		197.8	66% 1	32.9	61%	%86	52.4	40%			7077
55956.1			PF00054	PF00054	PF00125	PF00125		PF00099		PF00632	pir B38919 B38919	PF00096	gb AAD22522.1 AF0 91457_1	gi 4206088 gb AAD1	PF00096	gb AAC50252.1	_		_
protein [Homo sapiens]			PFAM: Laminin G domain	PFAM: Laminin G domain	PFAM: Core histones H2A H2B H3 and H4	PFAM: Core histones	H2A, H2B, H3 and H4	PFAM: Zinc-binding	metalloprotease domain	PFAM: HECT-domain (ubiquitin-transferase).	hypothetical protein 2 - human (fragment)	PFAM: Zinc finger, C2H2 type) zinc finger ZF [Rattus	(AF086837) snapin	ıger, C2H2		ZNF132 [Homo sapiens]		
			HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER	1.8	HMIMER	1.8	HMMER 2.1.1	blastx.14	HMMER 2.1.1	blastx.2	blastx.14	HMMER 2.1.1	blastx.2			_
			8860	9731	8871	9732		6688		8916		8928		8932	8934				
			899636	902517	937609	941948		915919		957580		961309		914667	909040				
			HDTBD67	HDTBD67	HDTAA31	HDTAA31		HDPXN01		HDPUN39		HDPSB10		HDPRR24	HDPRJ04				

538	377	377	574	377	574	377	538	377	553	377	574	377	553	377	538	556	377	371	553	571	517	377	553	538	371	194	611	611	611	611
335	18	12	335	12	335	12	335	12	335	12	335	12	335	12	380	326	12	39	335	380	335	12	380	380	93	51	513	570	534	573
47%	35%	34%	41%	34%	38%	31%	44%	78%	43%	30%	37%	31%	41%	31%	49%	36%	78%	30%	36%	35%	37%	27%	34%	33%	26%	33%	36%	20%	30%	%69
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611	611	611	611	599	365	611	354	611	371	276	576	490	646	582	187	83	700	774	788	746		797	411		226				445
534	573	573	582	513	303	513	292	573	327	544	544	200	530	523	155	700	771	803	823	417		414	262		366				287
30%	46%	46%	%09	27%	34%	30%	45%	46%	40%	45%	45%	42%	41%	%09	54%	%58	54%	100%	%99	102.12	-	78%	95%		87%	_			57.51
												gi 5080816 gb AAD3	9325.1 AC007258_14			pir JE0363 JE0363				PF00065		dbj BAA09322.1			gi 3694664 gb AAC6 2434.1	-			PF00433
									,			(AC007258) Putative	ATPase [Arabidopsis	thaliana]		mitogen-activated protein	kinase kinase kinase (EC	2.7) 1		PFAM: Neurotransmitter-	gated ion-channel	GABA receptor rho-3	subunit precursor [Rattus	Inol Vegicus	(AC004893) similar to NEDD-4 (KIA0093);	similar to P46934	(PID:g1171682) [Homo	sapiens]	PFAM: Protein kinase C
												blastx.14				blastx.14				HMMER	1.8	blastx		1.1	blastx.14				HMMER
												8939				8941				8959				0000	8989				8991
										_	,	922006				923120			1	973945				001701	921381				909833
						···						HDPQ168				HDPQF03			400	HDPLT62				UDD/2015	11DFG345	-			HDPGS16

			<u>~</u>	terminal domain				
	~		1-15-4-	(A TO 45700) A 1 . 0				
			blastx.2	(AJ245709) Akt-3 protein	emb CAB53537.1	100%	236	460
HDPFZ70	709684	9003	HMMER	PFAM: Core histones	PE00125	100%	5	116
			1.8	H2A, H2B, H3 and H4	6710011	13.3	700	(42)
HDPFB03	936331	9015	blastx.14	(AF043726) PHD-finger	gi 4529845 gb AAD2	38%	341	553
				protein [Mus musculus]	1792.1			
HDPDD12	970592	9017	blastx.14	(AF000998) CLOCK	gi 2114488 gb AAC5	%98	284	370
				[Mus musculus]	3200.1			
HDPCM62	454740	9031	HMMER	PFAM: Laminin B	PF00052	2.03	152	208
			1.8	(Domain IV)			1	2
HCWKR86	784705	6806	HMMER	PFAM: Zinc-binding	PF00099	2.26	296	340
			1.8	metalloprotease domain				•
HCWFA35	008820	9114	HMMER	PFAM: DnaJ, prokaryotic	PF00226	116.61	80	274
			1.8	heat shock protein	-		}	 i
			blastx.14	Curved DNA-binding	gi 1651491 dbj BAA3	%86	89	364
				protein cbpA [Escherichia	6142.1			
				coli				
HCUGN19	716989	9181	HMMER	PFAM: Alcohol/other	PF00106	8.05	86	151
			1.8	dehydrogenases, short chain type))	* · · · · · · · · · · · · · · · · · · ·
HCUGL20	668913	9184	HMMER 1 8	PFAM: Ank repeat	PF00023	7.2	190	261
TOENTOTO	0.4000	0,00	1.8					_
HCFING10	848772	9310	HMMER	PFAM: HMG (high	PF00505	6.03	305	376
			1.8	mobility group) box				
HCFMZ90	922112	9315	HMMER	PFAM: Beta-ketoacyl	PF00109	194.57	291	872
			1.8	synthases				<u></u>
			blastx.14	(AF021234) 3-oxoacyl-	gi 2522482 gb AAB8	57%	465	824
				[acyl-carrier-protein]-	1078.1	26%	255	494
				synthase [Neurospora		41%	91	306

	362	407	610	83	244	6	727		182	317	258	412	252		325		998)	953	893	185
	198	198	203	18	179	122	771		3	261	217	287	193		2		798		909	618	99
	55.5	42%	%68	95%	10.89	20.01	70.07		93%	100%	100%	95%	3.77		232.2		06	•	%89	33%	36%
	PF01772	gi 488750 emb CAA3 4890.11	gb AAF29005.1 AF1	61445_1	PF00125	PEOOOOA			gi 4093159 gb AAC9	9774.1		gi 438164 emb CAA8	PF00130		PF01283		PF00096		gb AAF03152.1 AF1	85576_1	PF00047
Cracsal	PFAM: Isopentenyl- diphosphate delta- isomerase	homologue of yeast IPP isomerase [Homo saniens]	(AF161445) HSPC327	[Homo sapiens]	PFAM: Core histones	PFAM: ATPases	associated with various	cellular activities (AAA)	(AF093403) 2-amino-3-	ketobutyrate-coenzyme A	ligase [Mus musculus]	Rab24 protein [Mus musculus]	PFAM: Phorbol esters /	domain	PFAM: Ribosomal protein	S26e	PFAM: Zinc finger, C2H2	type	(AF185576) POZ/zinc	JC -	PFAM: IG
	HMMER 2.1.1	blastx.14	blastx.2		HMMER	T.O HMMER	1.8		blastx.14			blastx.14	HMMER	1.0	HMMER	2.1.1	HMMER	2.1.1	blastx.2		HMMER
	9316		9321		9337	9355	_		9390			9415	9423		9437		9438				9452
	920506		955281		850426	781946			923730			912789	726475		849633		883006				835733
	HCFMW71		HCFMJ37		HCFCG23	HBTAE84			HBMTB85			HBMBF89	HBJNB52		HBJLR37		HBJLR31				HBJJX53

		157 216	215 283		201 371	181		931 1005		451 876					41 100		55 251	171		13 443		4 277				
-					,									916			135	145	 	423		444				
		%06	73%		64	1 57		13.48		20%	25%	33%	42%	43%	96'8	+ 00	1.75	2.72		3.09		48%	47%	43.4		
		gb AAD52965.1 AF1	61081_1		PF00046	PF00052		PF00054		gi 1857708 gb AAB4	8481.1				PF00027	DE00400	rr00400	PF00130		PF00099		gi 5802816 gb AAD5	1794.1 AF164612 1	PF00561		
(immunoglobulin)	superfamily	(AF161081) activatory	receptor PIRIIbeta [Homo	Saprens	PFAM: Homeobox	PFAM: Laminin B	(Domain IV)	PFAM: Laminin G	domain	contactin associated	protein [Homo sapiens]				PFAM: Cyclic nucleotide- hinding domain	PFAM: WD domein	beta repeat	PFAM: Phorbol esters /	diacylglycerol binding domain	PFAM: Zinc-binding	metalloprotease domain	(AF164612) Gag protein	[Homo sapiens]	PFAM: alpha/beta	hydrolase fold	
1.8		blastx.2		40.00	HMMER 2.1.1	HMMER	1.8	HMMER	1.8	blastx.14					HMMER 1.8	HMMFR	2.1.1	HMMER	1.8	HMMER	1.8	blastx.14		HMMER	2.1.1	1.1
		· · · · · · · · · · · · · · · · · · ·		0.45.0	9453	9461	- 1	9466							9472	9484	- - - -	9522		9524		9527		9532		
				34745	894343	930448		971377							923800	423885		660552		864344		930956		952057		
				UDIITIO	DBJJ112	HBJIH60		HBJHX73	1					COMPLETE	HBJG103 	HBJFC23		HBJAB15		HBDAD64		HBCCJ05		HBCBN51		_

ase fold; cDNA 03219.1 58% 57% 62% 45%	03219.1 58% 57% 62% 45%	ase fold; cDNA 03219.1 58% 57% 62% 62% 45%	ase fold; cDNA 03219.1 58% 57% 62% 62% 45%	ase fold; cDNA 03219.1 58% 57% 62% 62% 45%	429	69	525	717
ase fold; cDNA 03219.1	ase fold; cDNA 03219.1	ase fold; cDNA 03219.1	ase fold; cDNA 03219.1	ase fold; cDNA	358	7	478	658
ase fold; cDNA	ase fold; cDNA	ase fold; cDNA	ase fold; cDNA	ase fold; cDNA	28%	57%	62%	45%
hydrolase fold; cDNA EST 1	hydrolase fold; cDNA EST 1	hydrolase fold; cDNA EST 1	hydrolase fold; cDNA EST 1	hydrolase fold; cDNA EST 1	03219.1			
		,			hydrolase fold; cDNA	EST 1		

Table 2 further characterizes certain encoded polypeptides of the invention. [053] by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig indentifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide The fourth column provides the analysis method by which the sequences. homology/identity disclosed in the row was determined. The fifth column provides a description of PFam/NR hits having significant matches identified by each analysis. Column six provides the accession number of the PFam/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFam"), as described below.

The NR database, which comprises the NBRF PIR database, the NCBI [054] GenPept database, and the SIB SwissProt and TrEMBL databases, was made nonredundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than 1.0e-07, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent

identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[055] The PFam database, PFam version 5.2, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, (1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the positionspecific variation among the sequences that make up the multiple sequence alignment (see, e.g., R. Durbin et al., Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFam version 5.2. A HMM derived from PFam version 5.2 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFam family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFam hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which shows a significant match to a PFam protein family.

[056] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFam/NR database as disclosed in the fifth column of Table 2. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[059] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[060] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

Partial cDNA clones can be made full-length by utilizing the rapid [061]amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, Sall and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[062] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[063] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

Once a gene of interest is identified, several methods are available for the [064] identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be

used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase, if used, is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the immune/hematopoietic antigen of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant immune/hematopoietic antigen.

[065] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEO ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion

thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

- [066] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.
- [067] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into E. coli strain XL-1 Blue, also available from Stratagene.
- [068] Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus* 15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).
- [069] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed

sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

- [070] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of immune/hematopoietic associated genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [071] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [072] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.
- [073] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the immune/hematopoietic polypeptides of the present invention in methods which are well known in the art.

The present invention provides a polynucleotide comprising, or alternatively [074] consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEO ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEO ID NO:X. and/or the cDNA contained in Clone ID NO:Z.

[075] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine. ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B. column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic

acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[076] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention [077]comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEO ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[078] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the

invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[079] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[080] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to

the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

- In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- [082] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.
- [083] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower

stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[086] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10

polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[089] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3, 10 polynucleotides of

one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[090] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the third column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b; where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for

example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

Contig m.		EST Disclaimer	claimer Dange of b	,
961376	_	1 - 3744	15 - 3758	AI760827, AW408019, AI253155, AI349366, AI356482, AA814034, AW075920, AW407984,
				AI760691, AA251937, AI766650, AA352825, AA243541, AI934100, AA352840, H72208, H72106, AW193021, AL035530, AL035530, and AL035530.
573692	,	1 - 305	15 - 319	AL356513, AL356513, AL358796, and AL358796.
526312	1	1 - 375	15 - 389	AC006479, AC006479, AC006479, and AC006479.
958768		1 - 849	15 - 863	AI240823, AC012580, AC012580, AC012580, AL133502, and AL133502.
521835	,	1 - 89	15 - 103	AL133216, AC024998, AC024998, AL365438, AL365438, AL390122, AL390122, AL133216, AL133216, AL133316, AC032703, AC037703, AC03703, AC03706,
			٠	ALISSZIN, ALISSZIN, ACUZZINZ, ACUZZINZ, ACUZSINO, ACUZSINO, AFINONYO, AFINONYO, AFINONYO, and AFINONYO.
931477	1	1 - 553	15 - 567	AI908374.
964871		1 - 587	15 - 601	AL117337, AF205588, AL022345, AL022345, AL022345, AL161931, AL161931, AL161931,
				AL354975, AL354975, AL354975, AL355583, AL355583, AL355583, AL023808, AL023808,
100				AFZU3388, AFZU3388, AFZU3388, ALI1/331, ALI1/331, and ALI1/331.
864366	7	1-437	15 - 451	AA642815.
573989		1 - 415	15 - 429	AC021215.
669802		1 - 274	15 - 288	
503573		1 - 385	15 - 399	All 50061, AA382210, AC011448, and AC011448.
573993		1 - 224	15 - 238	AI114447, AL133243, AL133243, AL133243, and AL133243.
932514		1 - 657	15 - 671	AA312172.
861018		1 - 219	15 - 233	AB023431, AC005954, AC005954, AC005954, and AC068475.
922800		1 - 713	15 - 727	
935414		1 - 612	15 - 626	AA904376, H23157, AA663798, AA359944, AA448036, R61429, H09004, AA309011, AF126245, AP001785, and AP001785.
614849	_	1 - 375	15 - 389	AI057188, AW273323, C15735, AI932257, AI028587, AI940493, AW043720, AW021811,
				AA858079, AW197210, AI791278, AA508647, C15853, AA181800, AW043729, AW008982,
				A1918922, A1983340, AA031428, AA282283, AC00/392, 282198, AL031121, AL121840, 1.24095 AC004882 AC005539 AC003070 AC008984 AL133985 AL049781 773006
				AC005881, AL079305, AP000263, AC005888, AC003080, AC004935, AL035667, AC005610,
				AP000036, AC005186, AC004842, AL035696, AC003661, AC004503, AC009263, AL023581,
,				AC003009, U41096, AL021368, AP000567, AC004933, AC003975, AP000494, AL008638,
				AF015262, AL049833, AL034350, AL031010, AJ229043, AP001069, AC006288, AL049561,
	7			ALUZASO1, ALOUS/101, ALUOS/103, ALUOS/26, ALUZSZ83, ALUISSA, ALUIS

AL031684, AC008014, AP001038, AF064864, AP001037, AF165176, AC005993, AP001043, AL078602, AC007073, AL133512, AC005367, AC007751, AC004850, AC006928, AC009028, Z83823, AC003089, AL008715, AC007372, AL049837, AL078612, AF124730, AC006032, AF207955, AC008154, AL021395, AC005076, AC005886, AC008072, AC005036, AC004783, AC004002, AC006256, AL133485, AC006353, AC002485, AF205890, AC004106, AC004169, Z74696, AC006263, AC006384, AC006972, AL031767, AC006368, AC004158, and Z95152.	N47629.	AC003963.		AA313748, AC008013, AC006432, and Z61963.			AL133163,	AC002450.	AC004976.										AA766781, and AA352756.		AL117593, and AC007401.	AA249870, and AF205935.							AL078584.	
	15 - 510	15 - 808	15 - 439	15 - 248	15 - 518	15 - 321	15-315	15 - 119	15 - 401	15 - 300	15 - 290	15-320	15 - 345	15 - 363	15 - 201	15 - 460	. 15 - 230	15 - 304	15 - 341	15 - 332	15 - 232	15 - 415	15 - 537	15 - 277	15 - 388	15 - 530	15 - 100	15 - 228	15 - 461	15-512
	1 - 496	1 - 794	1 - 425	1 - 234	1 - 504	1 - 307	1 - 301	1 - 105	1 - 387	1 - 286	1 - 276	1 - 306	1 - 331	1 - 349	1 - 187	1 - 446	1 - 216	1 - 290	1 - 327	1 - 318	1 - 218	1 - 401	1 - 523	1 - 263	1 - 374	1 - 516	1 - 86	1 - 214	1 - 447	1 - 498
	725481	864338	557972	529753	722723	677397	953840	675904	527998	527908	828026	781398	527903	527112	714390	697628	823468	527711	847946	527702	531104	856216	752830	573846	494836	847935	932302	573728	919383	573847
	28	29	30	31	32	33	34	35	36	37.	. 38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57
	HBDAF51	HBDAF61	HBJAB59	HBJAC23	HBJAG72	HBJAI91	HBJAJ75	HBJAJ85	HBJAV57	HBJAY76	HBJAY91	HBJBM14	HBJBR94	HBJBU55	HBJCD43	HBJCD88	HBJCJ68	HBJCO81	HBJCR51	HBJCR90	HBJDL73	HBJDN14	HBJDO70	HBJDP32	HBJDP41	HBJDQ75	HBJDT05	HBJDT47	HBJDW23	HBJDW36

HBJDX18	58	795732	1 - 544	15 - 558	T94994, and AC007546.
HBJDX51	59	716395	1 - 391	15 - 405	
HBJEA22	09	674872	1 - 312	15 - 326	
HBJEA25	19	589249	1 - 498	15 - 512	AA912740, AA488771, T99916, AA370641, AA376428, AA488991, AA091598, D81695,
-					AA319426, AA224141, AW392797, AI240672, AA160646, AW403677, AL037869, AI240700, A 2314410, TI01377, AE002797, AE002796, AE002790, AE002797, AE002797, AE002797, AE0027900, A 2314410, TI01377, AE002793, and AE0026166
HBJEA44	62	973376	1 - 447	15 - 461	
HBJEA65	63	934994	1 - 543	15 - 557	T86098, and AL031589.
HBJEA90	49	895961	1 - 739	15 - 753	AA888592, AA489084, D80258, D80014, T11417, D59503, D59627, D81111, D58101, D80064,
					C14227, D58246, C06015, C14407, AI557751, AI535686, AI557774, AA514184, T03048, D51079,
					D80227, AW377671, C14298, D80269, D59695, D80168, D59467, AI535959, D50979, F13647,
					C14014, D80133, AA809122, D51213, D80188, D80522, D80043, D80378, D45273, D59502,
					D52291, D80195, AA305578, C03092, C15076, D80164, D59275, D80038, C14389, C14331,
					D80247, D80157, D81026, D51799, D80439, D51103, H67854, D80251, D58283, D80949,
		-	`	-	AASIHIBB, DSSBS, DSSBIV, DBVVZZ, DBVIBB, DSIHZS, DSPBIS, DBVZIV, DBVSIV, DBVSH, DBVZHV, DBVZHV, DBVZSS, DRVDHS, C14344 DS9787 DS0995 AA305409 DS9551 DR1030 DR0212 DR0268
			,	,	D80366, AW367950, D80196, D51022, H67866, D80219, AW178893, D57483, D80193, D59927,
-					D80248, D59889, D51759, D80302, AW360834, D51060, D59317, D80241, D80024, AA514186,
•					D59474, D45260, D60214, C14973, AI525237, AW177440, D51221, T03116, D59653, C14429,
				•	AW378539, AI525917, AW360817, C75259, AI525920, D60010, C14077, AW177505,
					AW375405, D59373, C14957, AI525227, AI525242, AW360811, C14046, C16955, C05695,
					AW178907, AI525923, AW178908, D80228, AI525235, T02868, AW366296, AW178906,
			٠		AW360844, Z33452, AA285331, T03269, AI525912, AW179328; T48593, Z21582, AW375406,
-					AW378534; AI525925, AI525215, AW179332, AW377672, AW360841, AW179023, AW178905,
-			•		AW1/7/31, AW3/8528, AW1/8/62, AW1/9019, AW3/8533, AW378532, AW352120, C05763,
		:		•	AW352117, 102974, AW377676, AW178914, C04682, AW378542, AW360855, AW178774,
					AW1/040/, N00429, D31033, AW1/9020, AW321/1, AW1/0900, AW3221/0, D31230, AW177733 AW378494 AW170034 AW349143 AF95799 AW170018 C13048 D31448
-	,			,	AW178781. AI535961. AI525928. AW378543. AW177728. AW369651. AW178986. AW177456.
			,		AW178911, AW378540, Z30160, AW178775, AW178909, AW179004, AW179329, AW179009,
					AW178754, AW352158, AI525228, H67858, AA305720, AW177508, AW177734, AW177497,
	,				AW179012, AI910186, AW177722, AI525216, AI525238, AI535665, AI525903, AB002449,
	,				AR016808, A82595, A84916, AB028859, AR060385, AJ132110, AR008278, AF058696, A62300,
					A62298, AR018138, I14842, AR054175, I50126, I50132, I50128, I50133, AR008277, AR008281,
_			-		X64588, X68127, A70867, AR062872, I82448, I79511, AR016514, X67155, Y17187, AR060138,
					A45456, Y17188, A94995, D26022, A26615, AR052274, A43192, Y12724, A63261, A43190,

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	1-161	1-511	1 - 413	1 - 65	1 - 410	1 - 291	1 - 411	1 - 414	1 - 323	1 - 363	1 - 320	1 - 249	1 - 608	1 - 648	1 - 258	1 - 650	1 - 276	1 - 350	1 - 320			1 - 484				-			
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HBJFW55	95	526682	1 - 259	15 - 273	AA283995, AI478915, AA283951, AI817564, AA283760, AA287165, AA286859, AA789104, and AC007068.
HBJFW68	96	573766	1 - 172	15 - 186	
HBJFW78	26	571347	1 - 380	15 - 394	
HBJFX57	86	573760	1 - 305	15 - 319	AL078584,
HBJFX81	66	529843	1 - 227	15 - 241	
HBJFY40	100	574095.	1 - 450	15 - 464	
HBJFZ21	101	671191	1 - 235	15 - 249	
HBJFZ40	102	526679	1 - 437	15 - 451	
HBJFZ56	103	507530	1 - 329	15 - 343	
HBJFZ82	104	799685	1 - 325	15 - 339	AW005281, and AA558937.
HBJGR59	105	739095	1 - 551	15 - 565	
HBJGT72	106	957668	1 - 354	15 - 368	R50003, and R50021.
HBJGT92	107	919507	1 - 722	15 - 736	T84928.
HBJGU70	, 801	864063	1 - 474	15 - 488	
HBJGU78	109	920821	1 - 568	15 - 582	AI553853, AW079768, AI683616, AI536991, AI254730, AI356243, AI630887, AI829696,
					AI889334, AI344419, AW411027, AI391729, AI926804, AI282481, and AC004031.
HBJGV17	110	662725	1 - 475	15 - 489	
HBJGV22	111	613781	1 - 280	15 - 294	AA382068, D54550, H62431, H13929, AW176445, H80318, AW374298, AA418306, D54133,
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					AA234625, AR064426, AB004/88, AF0/9221, AF06/396, and AL132665.
HBJGV32	112	699075	1 - 377	15 - 391	
HBJHG04	113	836184	1 - 419	15 - 433	
HBJHG76	114	970826	1 - 476	15 - 490	AC008282.
HBJHI28	115	686278	1 - 314	15 - 328	M62004, and AL035410.
HBJHJ44	116	621723	1 - 359	15 - 373	AA207226, AL121444, AA019182, AA333455, W96231, AA331923, H08904, AA446987, and AW167577
HBJHM50	117	724183	1-336	15-350	
HBJHM57	118	973257	1 - 419	15 - 433	
HBJHM76	119	715512	1 - 324	15 - 338	
HBJHN52	120	726570	1 - 334	15 - 348	
HBJH011	121	964943	1 - 522	15 - 536	AW006288, AA977097, AI368637, AW197236, AI341105, AI650705, AI816278, AI590528, and
					R44511.
HBJH060	122	975186	1 - 395	15 - 409	AL121820.
HBJHR56	123	686717	1 - 592	15 - 606	AA077952, AA482768, R96657, H79151, AW103981, AA169194, AA325699, M78177, AA626678, T69877, AA569387, AA332991, AA3249, AA326441, AA975645, AA357937.

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A143470 AA9738	AA4466	AL0399	N70103	AC0079	AC0044	AC0055	AC0050	AC0049	782198	AC0010	AC0050	AF1291	AC0078	AP0007		15 - 335	15 - 362 H68571,	15 - 650 AL117342	15 - 505	15 - 387	15 - 692 AA773280	15 - 338	15 - 429 AA5249	15 - 447 AA864727	15 - 428 AC007564,	15 - 541	15 - 538	15 - 413	15 - 489	15 - 438		15 - 344 AC0024
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AR050541.		AC007488.		AC007319.	N27511.	AI886860, R17495, H96146, AA582791, AA069643, W02625, AA745628, T51436, AA593092,	AI955111, AW169038, AI538214, N32496, AA243974, AA244061, AA629731, AA737235,	AA745653, AI343169, W24944, H39038, AA856904, AA324108, T62233, AA279649, AA188676,	AW410201, AI671077, W03120, AI570237, AA187624, AW404337, AA848002, AI418661,	H81267, AA229422, F23294, T26476, AA523695, AA032001, AW341741, F30158, R32162,	AA179304, AA452325, AA668715, AA215470, AC004644, AC006111, AC005618, Z95331,	AC006146, AC002312, AL021918, AC005089, AC005086, AC002381, AL031295, AC004687,	AC008101, U91322, AC016027, AC005874, AF134471, AC016830, AC005081, AF047825,	AC006449, AC007425, AL049709, AL132777, AC005730, AC002352, AL031311, AC009946,	Z83819, AC003108, AC004970, AC003982, Z98884, AC005969, AC006006, AL121658,	AC005015, AC008079, AC004216, AC005193, AC007546, AC007731, AL139054, AC006241,	AL121825, AC006312, AP000504, AL133485, AC005500, AC004794, AC002544, U95739,	AC003098, AP000103, AP000032, AL133243, AL021155, AF129756, AC004253, AC006581,	AC005921, AL035681, AL022165, AL109758, AC007227, AL021391, AF111169, AC006130,	AC005666, AF196972, AC007537, AL096701, AL050332, AL022334, AL096678, AC006084,	AP000216, Z98751, AC002301, U15422, AL034402, AC006251, AC003037, AL035684,	AL034418, AC005006, AL121653, AF196779, AC006211, AL078593, AC005531, AC005237,	U73634, AC007566, AC002126, AF064861, AC005562, Z83843, AC002565, AC006040,	AC000379, AL021026, AC005018, AL035460, AC005317, AC007376, AC004883, AC005037,	AC004821, AC005971, AF001550, AC002404, AL109865, AC005207, AL031584, AC000035,	AC005332, AC004938, AB020864, AL133163, AP000694, AC003661, AF003626, AC005486,	AP000516, AC004876, AL035086, AL135744, AC005815, AP000514, AC005663, Z98752,	. AL049780, AC007055, AC006441, AC005377, AC008372, AC009510, AL031778, AC005664,	AF111168, AC005907, AL031281, AC005620, AL021707, AF126531, AC020663, AL022302,	Y14768, U91321, AL109967, U91327, AC000025, AC006160, AC004386, AC007052, Z83826,	AC005544, AC007011, AL031673, AC004150, U63630, AC003072, AC007686, AC005048,	AC006132, AP000553, AF195658, AC004542, AC002316, AL022336, AF053356, AP000043,	AP000111, AC004647, U91323, AC005082, AL133448, AL109952, Z97055, Z93017, AP000030,	U07000, AC005768, AC019014, AL049832, AC007774, L78833, AC003119, Z84480, AC002365,	AL121655, AC004223, AC005839, AC000353, U80017, AC005325, AL020997, AC005829,	L78810, AC005632, AC005821, AL035413, Z69719, X69908, AC004933, AC002310, AC004983,
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					AA483929, AI499588, N57739, AA664548, AA493136, AI524360, AI791913, AI821714,	AA482273, AW023990, T06754, AA455670, AA630672, AA501649, AA961035, AA579179,	AA837087, AA533782, AA487888, AW438542, AA503298, AI821785, AW023149, AI223700,	AW149313, AA588001, AA618452, AI473475, AA662976, AW270343, AI933714, AI431240,	AA858372, AW148507, R31790, AA857370, AW196064, AA339692, AA580808, AA864261,	AA502991, AW238605, AA370455, AI580250, AA507282, AI648410, AI587224, AA483771,	AW270709, AA595499, AA516233, AA828062, AA501852, AA719073, AI470646, AA846935,	AA297666, AI859438, N23504, AI683446, AA436774, AL138096, AA002063, AA635368,	AL042927, AI874308, AA654661, AA610688, AA436782, R23521, AA515905, AA502440,	AI696595, AA071334, AA621381, AI921043, AA468505, AW341978, AI792133, AA230213,	AA643770, AA651632, AL036037, AI354388, AI754544, AA707782, AA707705, AI341571,	AA833896, AA282820, AA833875, AI733856, AA780944, AA503119, AI754567, AA483223,	H25921, A1755214, R23441, A1691091, AA493975, AA368573, AI056177, AA522642,	AL038971, AA513893, AA653375, AL044586, AA687535, R73754, H29019, AA634837,	AL047429, AA209423, AI587565, AI587583, AW302080, AI253007, AW081194, AW302087,	AI434695, AA077019, AC004257, AC005696, AC016830, AC005060, AC006313, AC005071,	AC003070, AF111168, AL049779, AL031447, AF047825, AC004659, AC006120, AC004148,	AL133246, AC016027, AC007191, AC005002, AC005527, AP000556, AP000252, AC003029,	AP000552, Z82180, AC003690, AC005226, AC004832, AC004883, AC005581, AC005387,	AC004999, AL121653, AC004884, AC006312, AC005519, AC007842, AC005003, AL033518,	AP000557, AL096701, U82828, AL049653, AP000703, AL121595, AC006251, AP000116,	AP000049, AC007277, AC004638, AC005914, AL035422, AL050318, AC005880, AP000121,	AP000053, AC005939, U47924, AL110502, Z97054, AC006112, AC005317, AL135744,	AP000311, AC003663, AL049761, AC004953, AC004019, AC002116, AC005694, AC006487,	AC005512, Z95115, AL021807, AL049745, AC007011, AC002301, AC005231, AC002375,	AC006978, AP000066, AP000558, AC012384, AL109984, AC005197, Z75746, AF001549,	AL031228, AC004814, AC006285, U82668, AP000513, AC005529, AL021940, AC005971,	AC002310, AC006208, AP000244, AF111169, AC005899, AC005280, AC005049, AC006441,	AC002531, AL049776, AC020663, AC007172, AL022165, AC004675, AC005031, AP000251,	U91326, AC004149, AC003024, AF165926, AC006530, AJ003147, Z85999, AL023553, L77570,	AL049589, AC009247, AC005305, AC005790, AL109798, AC007193, AC005730, Z84483,	AL034451, AC002492, AC004983, Z84466, AC004706, AC007450, AP000355, AC005181,
15 - 488	15 - 240	15 - 287	15 - 305	15 - 343	15 - 354							,				-								_												
1 - 474	1 - 226	1 - 273	1 - 291	1 - 329	1 - 340																							_		_	_					
735748	864013	952791	656721	665874	847840	-				-				-,								•														
177	178	179	180	181	182																															
HBJLE82	HBJLF58	HBJLL07	HBILL13	HBJLL18	HBJLL28		,		-										•• ,				,										٠			

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AF088219, AC006581, AC002543, AP000065, AC007546, Z93942, AC005856, Z85996, AL088219, AC006581, AC006581, AC002409, U89335, AL031673, AP000030, AJ133269, AC0046812, L44140, AC000159, Z98036, AB023052, AF196969, AJ010770, AC002470, Z83844, AC004686, Z82214, AC000134, AC003982, AL078477, AC009516, AL035420, AP000692, AC016831, AC005399, AC009399, L78810, AC005531, AC00025, AL049757, AC004833, AC004655, AL049699, AL033543, AC006137, AC002041, AC00025, AL049757, AC004383, AC007387, U91323, AC007277, AP000512, AC007262, Z98884, AL133448, AL049759, AC007114, AL033522, AF043945, AC006211, AC007656, AC004955, AC004263, AF129756, AL022721, AC005598, AL031255, AC005765, AL049872, AL031983, Z85986, AL035684, AC007371, AC008040, AC008132, AC005037, Z83846, AL023807, U80017, AC002472, AL133163, AC007919, AC006453, U91325, AC005520, AC005940, AC000353, AC005209, AC004448, AC00686, AC006009, AC016026, AC002996, AC007887, AC006026, AC005081, AC004448, AC007686, AC006040, AC016026, AC002395, AC004848, AC006234, AC006006, AC016026, AC002395, AC004848, AC007686, AC006040, AC016026, AC002395, AC004848, AC006234, AC002070, and AL139054.				AA075481, AA075480, AA075067, AI791780, AA127140, J04716, L39879, L01122, M73706, S89400, K01930, J02741, U75408, W38303, AA076112, and AA076111.	AW239537, AA232075, W78769, AW020962, AA448818, AA128583, and AJ010842.	AI797543, AA121152, AW189950, AA281969, AI082147, AI034184, AI871347, AA815173, AW418773, AA579808, AI468532, AI290248, AA458860, AA227296, AA573302, AA702437, AA278877, AA227295, AI458479, AI802340, T07432, Z39708, AI985569, T85327, AA659414, AI027853, AI766719, AA350191, AA904439, T16811, and AC004798.	T87986, and AA814273.				AW206211, AF150250, C14388, AC002045, AC009509, AC006241, U52111, AC002554, AC004491, AF047825, AC005086, U95739, AF111168, AC007285, U80017, Z82190, AL031602, AL121655, Z97054, AC004893, AC005874, AF134471, AC007993, Z85987, AC003104, AC000134, AC007919, AC004692, AC008115, AC005363, AC005822, AC005300, Z94801, AC002128, AC003029, AL034429, AC005088, AC005914, U96629, AC005534, and M18157.		AA126910, AP000360, AC000053, AC002060, and AC005002.
	15 - 336	15 - 346	15 - 355	15 - 896	15 - 368	15 - 388	15 - 660	15 - 193	15 - 468	15 - 545	15 - 481	15 - 440	15 - 393
	1 - 322	1 - 332	1 - 341	1 - 882	1 - 354	1 - 374	1-646	1 - 179	1 - 454	1 - 531	1 - 467	1 - 426	1 - 379
	734522	752810	657747	843811	779004	823400	661665	725095	726491	760155	975088	792110	675692
	183	184	185	186	187	188	189	190	191	192	193	194	195
	HBJLL57	HBJLL68	HBJLP14	HBJLR56	HBJLR82	HBJLV29	HBJMA30	HBJMA51	HBJMC53	HBJMD71	HBJMD74	HBJME92	HBJMF23

			AW182540, AA610084, AI936489, AA306791, AW340569, AA905749, and AB033050.	AW004683, H87822, H87851, and AW015156.	AC004254.	AL031657.	AI241023, AW401921, and AB023483.	AC002368.	H55415, W22115, AL096701, and AB011114.		AA601336, AA640305, AW341878, AI567676, H79323, AA593168, AW020612, AA167656,	AW085626, AA729004, N27362, F35374, N49298, AA179364, W45416, AI520984, T89141,	R99617, AI253347, AI918661, AI061158, AI281622, AA947352, AA228268, AA664963, W27084,	AA761454, F01694, T57636, AA299490, AI744890, N63562, AI640905, AI919048, H81012,	AI569452, AA828840, AI828721, AA496042, AW028376, AI343808, AA776663, AA428991,	AI363336, AI149177, AL049743, AF165926, Z83840, AL109984, AL031311, AC005412,	AC004821, AC007686, AC007546, AC007207, U85195, AC005377, AC007421, AC008115,	U95742, AE000658, AC004832, AL035587, L78833, AC007216, AL020997, AL031589,	AC004797, AC005520, AL035420, AF196779, AF139813, Z98200, AL033392, AC003025,	AL035086, AL080243, AL121655, AC006530, AC005355, AC002312, AJ246003, AC004228,	AC004895, AC005180, AL096791, AC006312, AP000512, AC005519, AC006285, AC005081,	AL049869, Z82190, AC005839, AC005015, AL049694, AC004816, AC006071, AC005726,	AC002120, AL031293, AC005089, AC0066121, AL021453, AC005527, AC005696, AC006139,	AL135/44, AL133163, AF21/403, 29/630, AC0039/1, AL035422, U/802/, AC0048/8,	AC004975, Z82176, AF023268, AC000025, AL121603, AL008582, AL049757, AF001549,	AC005399, AC005914, AC007387, AC005207, AC000048, AF207550, AC005821, AC002094,	AP000248, AC005876, AC002117, AC005231, AC005288, AL034429, AC006130, AF111167,	AP000704, AL133448, AL096701, AC007386, AF111168, AC005529, AL031280, Z98884,	Z73979, AF134726, AC004099, AC006581, AF051976, AC006160, AC006077, Z93020,	AC004212, AL008734, AL031655, AC007993, AC005695, AP000555, AC004913, AC007308,	AF109907, Z97056, AC005277, AL020995, AC003041, Y18000, AL117329, AC007263,	AL034421, AP000503, AP000008, AC004967, AP000514, AC004834, AC002558, AL034420,	U52112, AC005632, AL022333, AC005755, AL049780, AL031123, AC007055, AL133246,	AC005911, AC005049, AC003109, AD000092, AC004897, AC007226, AC005183, AC005829,	AL023807, AL122020, AL109952, AD000864, and AC005993.	
15 - 580	15 - 388	15 - 439	15 - 457	15 - 452	15 - 479	15 - 676	15 - 422	15 - 462	15 - 527	15 - 507	15 - 615		(ě				-						15 - 254
1 - 566	1 - 374	1 - 425	1 - 443	1 - 438	1 - 465	1 - 662	1 - 408	1 - 448	1 - 513	1 - 493	1 - 601			,					,	,																1 - 240
691179	720050	720047	935952	794129	614911	864004	760833	090669	576429	964484	740142														•										\dashv	726480
196	197	198	199	700	201	202	203	204	205	206	207								ı	,								,		:						208
HBJMF30	HBJMF47	HBJMI76	HBJMK34	HBJMK94	HBJML28	HBJML69	HBJMM72	HBJMN75	HBJMQ86	HBJMR15	HBJMR60											,	•													HBJMT52

		AI810024, AW023610, and AA609969.		AW166629, AA601349, AA052895, N66744, AI732437, AII14704, T86740, AA491447, T98482, AA918759, AA663115, AA663086, AA291630, H72049, AW084938, R11040, AI926873, AW440498, T87973, AA846969, H93001, N63743, AA603883, AW028174, AA833162, AA507035, AA706845, AA837385, AA291700, AA297496, H73336, AA352365, AC004961, AL133382, AL034411, Z73420, AC002352, AC004887, AC003108, AC004645, U91326, AC006111, AC005509, AC004081, AL008712, AC016831, AL031276, AL033392, AC005531, AC007298, AL080286, AC004950, AL031985, AC004987, AC004448, AP000365, AL021939, AP000295, AP000044, AP000112, AP000152, AC004231, AC00563, AC006549, AF001549, AC005516, AC004466, AC002312, AC002390, Z92547, AC005746, AC003071, AC002544, AI010770, AL031584, AL121595, AB014080, AF017104, AB026898, AL049430, AC006059, AF147316, AC005081, AC004638, AC004876, AC004106, AL022578, AC002365, Z85987, AF196779, AC007364, AC004167, AL034582, AC016027, M98447, U82671, AL009179, and AP000553.				AA985391, AI053911, AA548890, AW403888, AL037632, AA081462, AI470646, AA834809, AA588001, AA833896, AA833875, AI580250, AA912287, AA483771, AA380354, H59372, AV274349, AW303196, AA580808, AW196064, H61630, AW301350, AL138096, AA515457, AI791913, AI792133, N54894, AI821714, AA679154, A1282511, AA483218, F25733, AI270096, AL119713, AL120687, AI283312, AA679154, AI282511, AA483218, F25733, AI270096, AL119713, AL120687, AI283312, AA683258, AA507822, AA457642, AA491862, AA491850, AC005815, AL008715, AC005036, AC008055, Z98941, AL096772, AC023172, AC005144, AC006013, AC007435, AP000201, AP000091, AP000093, AC007488, AP000088, AC005722, AC002480, AL0249712, AC002523, AP000001, AP000097, AP000237, AF107258, AC007437, Z74739, Z86064, AJ229042, AC005261, AF001552, AF146191, Z83846, AC007842, AL009050, AC007671, AC005249, Y12853, AC007298, AL023807, AC004216, AC008372, AC005284, AC004741, AL121595, AC002499, AL021978, AC005874, AF134471, AC005146, U91323, U82668, AC002536, AP000966, AC007262, AL033379, AC004948, AL080239, AC002091, AC007681, AL049744, AC010200,
15 - 483	15 - 657	15 - 352	15 - 367	15 - 361	15 - 396	15 - 530	15 - 355	15 - 781
1 - 469	1 - 643	1 - 338	1 - 353	1 - 347	1 - 382	1-516	1 - 341	1 - 767
952862	669030	614930	933143	690404	703843	809996	786707	576434
209	210	211	212	213	214	215	216	217
HBJMV72	HBJMW20	HBJMX04	HBJMX21	HBJMX29	HBJMX34	HBJNC11	HBJNC89	HBJND59

AI345397, AI627714, AA207067, AI955945, R65859, AI560227, AI335235, AW021373, AI699056, AI285419, AI273856, N99092, AL047422, AI434731, AA127565, AI336631, AW072719, AA642348, AW190242, AI539690, AW079768, AW268302, AW235501, AA768478,	AI583982, AI337186, AW302954, AW104141, AI348854, AI002285, AI050666, AI307494, AW274355, AI250646, AW088899, AA176980, AI336582, AW167229, AI251221, AI349957,	AW131952, AA653459, A1285439, AW161579, A1885949, A1582871, A1581033, A1224463,	W48671, AI340511, AI624304, AA857847, AI679959, AI633061, AW022494, AI348870,	AI571699, AI699154, AW020288, AI702527, AA420722, AI349814, AI349186, AI336575,	AW020710, AW023859, AI609375, AI349772, AL038463, AW020397, AI334895, N63128,	AA579232, AA635382, AW082835, AI815232, AI335476, AI343030, N33175, AI471909,	AI491904, AI284517, AW268964, AI379711, AI218156, AW243232, AI804505, AI866581,	AW075382, AI859644, AA629977, R32821, AW020826, AA062896, AI927233, AI348895,	AI656270, AW068845, AI698391, AI336495, AI349276, AI538564, AI784214, AI612885,	AI345639, AI553645, AW191003, AW089122, AI915291, AI371251, AW152182, AI538850,	AI859991, AI537273, AW148303, AI582932, AA514684, AW020373, AI590043, W38903,	AIS86931, AIS24179, W46378, AI446775, AI690946, AW088560, AW301344, AI521560,	A1889189, AW264727, AL036146, AW161202, AW172723, A1309306, AI473536, A1866461,	AEG45020, AW 121972, ALGOUGG9, ALGOUTTO, ALCOUGG9, ALCOUGT7, ALCOG97, ALCOUGT7, ACC4518, ALCOUGT7, ACC664718, ALCOUGT744	AL137562, AL137712, AR068466, E12579, AL117440, S77771, AR038854, AL133093,	AF043642, A08913, L04504, U89295, A08912, X06146, E12580, AL133606, A08910, E01573,	E02319, A18777, A08909, AL049324, X99257, X57084, U80742, S76508, AL137276, A08908,	S36676, AL122123, AL080074, A08907, L40363, AF090886, S69407, AL049452, AL110196,	U90884, AL133081, AL137273, X93495, AL117432, AL110280, AC006197, AR050959, I89931,	133391, AL110197, AL049460, AB030279, 189934, X00861, 149625, AF026124, AF058921,	AF150103, AR064250, AB019565, AJ131955, AL133636, AL050280, AB025103, AF079763,	E00984, I04527, X62773, AF008439, I89947, A65965, L13297, Y11587, A65943, AL050155,	E03671, AF200416, AF017790, I30339, I30334, I48978, AL096720, AF090896, AL133565,	AF114168, AL008706, E08516, E02152, X63410, S75997, AL137429, AF100781, A90848,	X62580, U67328, AR029490, I46765, AC006313, AB007812, U96683, X86693, AL080147,	AF016271, E01614, E13364, U91329, AL137292, AJ012755, U72620, 189944, AF026816,	AF169154, X82434, X79812, A65341, I42402, AF031147, M86826, AF106697, AL080158,	E01314, AL122100, 166342, S83440, U62966, AL133113, AL133010, AF137367, AL137555,	U75370, AF047443, AF032666, X72889, AL137550, AF001552, L24896, AF115410, U75932,	AF091084, AL133104, AF175903, AL117644, AR054987, Y11254, AF141289, AL137538, AL133557, AL133016, AF036268, U57352, AL080132, AL080137, Y10080, AL137548
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	15 - 325	15 - 333	15 - 421	15 - 1289	15 - 518	15 - 301	15 - 458	15 - 289	15 - 358	15 - 453	15 - 576	15 - 401	15 - 507	15 - 267	15 - 689	15 - 500	15 - 326	15 - 528	15-317	15 - 345	15 - 383		15 - 448
	1-311	1 - 319	1 - 407	1 - 1275	1 - 504	1 - 287	1 - 444	1 - 275	1 - 344	1 - 439	1 - 562	1 - 387	1 - 493	1 - 253	1 - 675	1 - 486	1 - 312	1 - 514	1 - 303	1 - 331	1 - 369	!	1 - 434
	531494	698362	574803	880580	716647	736084	793174	847826	723005	674659	932037	711318	495736	658484	703438	465070	751643	529580	660/96	683436	855694		691116
	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255		256
	HBMBU38	HBMBX69	HBMBY27	HBMBZ71	HBMCA44	HBMCA58	HBMCA94	HBMCD26	HBMCD49	HBMCE22	HBMCH75	HBMCH88	HBMCK57	HBMCQ14	HBMCS34	HBMCS77	HBMCT67	HBMCU92	. HBMCZ11	HBMCZ27	HBMCZ32		HBMDA51

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HBMTW58	280	806670	1 - 651	15 - 665	
HBMTX29	281	689834	1 - 139	15 - 153	
HBMTX84	282	537385	1 - 338	15 - 352	Z93017, and AL009181.
HBMTY82	283	523728	1 - 316	15 - 330	
HBMUA62	284	557828	1 - 330	15 - 344	AI064768, Z98753, AL031681, Z95703, AC000354, AC007036, AL135746, AL109653,
		-			AP000516, U82672, AL133512, AL049648, AL033530, AC004986, AC002357, AL049554,
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					AL096803, AL021812, AC002069, AC011604, AF121898, AC005323, AC006354, and AC004930.
HBMUD12	285	574796	1 - 306	15 - 320	AL122020.
HBMUF60	286	740606	1-311	15 - 325	AC007536,
HBMUG57	287	735024	1 - 303	15-317	
HBMUH62	288	752244	1 - 329	15 - 343	AL096791.
HBMUJ84	289	531159	1 - 243	15 - 257	AI312718, AC005023, Z95118, AC005041, and AL034548.
HBMUK59	290	712591	1 - 462	15 - 476	
HBMUN30	291	693337	1 - 559	15 - 573 ·	AF015720, AJ229041, AC005829, AL031283, AC000134, and AL031255.
HBMU010	292	953933	1-316	1,5 - 330	
HBMU012	293	417210	1 - 178	15 - 192	AL022313.
HBMU090	294	928078	1 - 311	15 - 325	
HBMUP35	295	531101	1 - 236	15 - 250	
HBMUT83	736	793052	1 - 462	15 - 476	AW080842, AI126237, AA033525, AI288602, AA070152, AI200312, AW293916, AI738708,
	;	,			AA033526, AW182578, AA961647, AA808104, AA884100, AA410505, AI635980, AA580797, A A 748547 T71568 A TO14853 A A 975024 A 1674097 A A 988905 T82022 A I 133609
,		,			AL137420, and Z94722.
HBMUV03	297	924916	1 - 394	15 - 408	
HBMUY32	298	896656	1 - 234	15 - 248	
HBMUZ96	299	574522	1 - 208	15 - 222	AL020995.
HBMVA83	300	529815	1 - 275	15 - 289	AL043165.
HBMVE14	301	545170	1 - 685	15 - 699	AA160290, AA357550, AW377670, AA046565, AA447158, W42824, and N21687.
HBMVI79	302	781686	1 - 227	15 - 241	AC020663,
HBMVI94	303	574511	1 - 191	15 - 205	
HBMV002	304	920759	1 - 598	15 - 612	AL109839.

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HCFAY33	345	576058	1 - 166	15 - 180	AC005969.
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	960925	180915	576094	276098	260925	506251	216667	506250	953522	805822																			954213	933017	664132	772262	576446
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HCUAL07	449	923876	1 - 442	15 - 456	AI919285, AI091391, AI143678, AW152653, H92931, AW243238, AI863952, AI263430,
					AI308855, AA814965, AF079098, and AF079099.
HCUAM57	450	574375	1-313	15 - 327	T91791, AW071109, AI087055, AA338281, AA225175, AA525157, AA973913, AI348567,
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HCUAM95	451	727174	1 - 243	15 - 257	AA613766, Z82901, and AL136520.
HCUAN44	452	574154	1 - 499	15 - 513	AA985143, AL133245, AC009239, AP000500, Z97183, and AL020997.
HCUAN49	453	577897	1 - 163	15 - 177	AA651923, AA765019, AA668900, AA968447, and AC004968.
HCUAN72	454	850140	1 - 191	15 - 205	AL049709.
HCUA003	455	924902	1 - 311	15 - 325	AA595705, AI886736, AA765409, AC005011, AF196971, AC006530, AC005520, AC006236,
-					and AB020875.
HCUA028	456	850062.	1 - 334	15 - 348	T94088.
HCUAQ92	457	889905	1 - 279	15 - 293	
HCUAR07	458	953872	1 - 147	15 - 161	AW167136.
HCUAT07	459	698856	1: - 484	15 - 498	AL042660, AA633908, AI791151, AW339562, and AL021396.
HCUAU02	460	920694	1 - 140	.15 - 154	
HCUAU16	461	574193	1 - 294	15 - 308	
HCUAX57	462	934633	1 - 294	15 - 308	AI243475, AW183326, H22954, and F04138.
HCUBB28	463	685493	1 - 225	15 - 239	AA569686.
HCUBB46	464	577238	1 - 327	15 - 341	

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			HCUBK36	HCUBK39	HCUBK46	HCUBK49																												

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	739021	577291	953879	577287	971421	664536	926656	526757	850016	575352	967074	522378				,			577286		٠,
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	HCUBZ37 HCUBZ86 HCUBZ86 HCUBZ88 HCUBZ88 HCUBZ88		920682 574239	615547	506518	529702	694720	574096	506585
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	1580		HCUBT02 HCUBT94	HCUBV04	HCUBX57	HCUBZ57	HCUBZ86	HCUBZ88	HCUBZ96

HCIICB20	507	574189	1-415	15-429	AT 031295 AC002316 and AC005696
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					W21218, AW090629, AI962050, AW023975, AL135643, AA659083, AW419262, AI751162,
					AW162288, AI917271, AI307201, AI431303, AI688846, AI284640, AI471481, AA657741,
					AW029038, AI696793, AI345654, F36273, AW166815, AW193265, AA527954, AI350211,
				- 180 ₁	AL041854, AI904894, AL138421, AW193432, AI918421, AI653886, AC004821, S77605,
				•	AC006312, AL008715, AF165926, AC006960, AC005412, AL008635, AC004491, AC002449,
			,		AC009225, AL031670, AC008009, AC004985, AC005874, AF134471, AC004382, AC004675,
			. ,		AF088219, AC004797, AC005220, AL109801, AC003681, AF205588, AC020663, AC006111,
					AL035587, AC006992, AC007676, AL034376, AC005696, AC005695, AL035086, AF003626,
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			,		AL031584, AC004972, U62292, AP000346, U82671, AL096791, AJ251973, AC005034,
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-	_				AC006251, AC005702, Z70288, AC005514, AL132987, AC004678, AL022334, U02054,
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	,				AL132712, AL031281, AC004883, Z69890, AL096701, AL049830, AC007216, AC003065,
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					AC004216, AC007055, AL031005, AC000075, AC005033, AL109613, U73168, AC005330,
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					and AF134726.
HCUCC78	509	577129	1 - 291	15 - 305	AL022318.
HCUCC96	210	796530	1 - 229	15 - 243	AW005018.

AB020868.	R22017, AC004787, and AF165926.		D60319, D60589, D60408, D61144, D60853, AF119569, AF091501, and AF087651.	AC007032.						AA936845, N73060, N73203, R14903, AA988600, AA595504, M78131, AA774006, W68328,	H15294, AI049504, AA364863, AW131417, AA077619, AA477517, H53101, AA665304,	AA457230, N57709, AL037006, R38509, H58786, AI791561, AA173334, AA525407, H10454,	R48980, AA636102, AI479068, AA225548, AA321595, N22153, AW192518, R82835,	AW073498, H09639, A1929410, AI753672, AW019964, AI750950, AA693806, AA629412,	AA479337, AI273675, AA296958, C14599, AI268564, AA706094, AA831801, C14880,	AI138918, AA741020, AI367222, AA832016, AI371804, AI860535, AW276933, H63220,	AW103407, R83708, AC009399, AP000128, AP000206, AP000245, AC005529, AL008715,	AL034420, AC000025, AC005527, AC009247, AC004531, AC002407, AP000688, AC011331,	AC002990, AC004466, AL008718, AC004540, AL031803, AC002381, AC006077, AC005351,	AC005901, AC005822, Y11107, AC000086, AL133275, AC004910, AC006042, AC007919,	AC006417, AF006487, AC004383, Z99716, AF111168, AL035587, AC005972, AL031577,	AC006275, AC002301, AC002351, Z97054, AC007055, AC007537, AC002120, AC005291,	AL031428, AF027974, AC000353, AL034419, Z95331, U72845, AC004955, AL031255,	AC005088, AC004587, AC002563, AL133448, Z85986, AC005209, AL109963, AC007263,	AC005480, AC007540, AP000116, AC005231, AC006388, AC000066, AC004000, AC005049,	AC004851, AL035415, AC002073, AF134726, AC009509, AC005585, AL021154, AL118516,	AC007227, AC007201, AC005071, AL096775, AC005740, AC005921, AP000555, AC004983,	AL121915, AL049766, AC004139, AL049830, AC007226, AC004908, Z98752, AC007536,	AC007559, AC004036, AC005037, AC005578, AF092925, AC006059, AC005486, Z98941,	AC007028, AJ010770, AC005064, AL078581, AC008249, AC007214, AC002072, Z82178,	AC005796, AL109952, AL009181, AC005971, AC010168, AL033527, AC004054, AL049699,	AD000812, U91324, AP000252, AL024498, AC003962, AF141308, AC006449, AL034418,	AC008044, AL021578, AC005722, Z84474, AC005521, AC005479, AL033524, U91318,	AL031685, AC004694, AC007899, AC004125, AC005399, AL121825, Z74739, AC006344,	AC005005, AL035422, AL133249, AL023581, AC006071, AC004019, AC005821, AC000026,
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-		15 - 393	15 - 168	15 - 1810					•		15-277													•		,				-
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	583	584	585	286	
	HCUE031	HCUE041	HCUE062	HCUE079	

AC004967, AC005206, AC005667, and AC005519.	AL008718.	AW452694, and AA972635.		AA084609, AI312309, AI678287, AW151848, AA757621, AL037927, AI962030, AI306717,	AWU841/3, AI30/U/0, AA98492U, AWU23389, AW4U2/84, AIU03U31, ALU42/33, AW 236493,	A1186233, AA825827, AA496309, AA584655, AA747575, AA584756, AI689135, AW192179,	H29914, T67090, AI303008, H40478, AW328027, AA551548, AL078581, AC007199, AC005821,	AC005736, AC005081, AC005722, AC007285, AC005520, AL049301, AL049538, U80017,	AC002477, AC020663, AL031311, AL021453, AC005015, Z69921, AF129756, AC000120,	AC002314, AC006530, Z69653, AP000065, AL035400, AC005519, AP000512, AB001523,	AL117258, AF207550, Z98742, Z99128, AC007225, AC004858, AC006146, AC005696,	AC007386, AL133245, AP000121, AC007686, AP000045, AC007363, AC000041, AC002115,	286090, AP000704, AC002350, AC005102, AL049697, AC005057, AC007537, AF064861,	AC002306, AC005280, AC004560, AC003957, AL031602, Z98941, AC005899, AC005837,	AC005488, AC002059, AC000353, AC004622, U91326, AC004531, Z83856, AP000688,	AF111167, AC004967, AL022316, AC002544, AC005746, AC004841, AC000118, AF001548,	AC005682, AL049758, AC005220, AC003041, Z93930, AC007327, AC006312, AC004796,	293244, AC004685, AC005829, AB003151, L44140, AC004962, AC004659, AC005562,	AC007868, AC004408, AL096701, AC005049, AC004019, AC005500, AL023553, AB014079,	AF165926, AL078463, AC009509, AC004477, X64467, AC006026, U63721, AC006120, L77570,	AC004263, AL009179, Z95152, AF111168, AC004491, AC007240, AC006023, AF053356,	AL022326, Z97054, AC007731, AC001231, AC005484, AC003982, AC005094, AC004686,	Z83844, AP001058, AC000159, AC007367, AL031985, AC005412, AL049843, AC006538,	AL021917, AF045555, AC006077, AL031295, AC003029, AC004383, AC002039, Z81364,	AP000008, AC002492, AP000208, AP000130, AL096791, AC004148, AP000355, AF196969,	AC002312, AL031662, AP000556, AL139054, AC007637, AC006111, AC005387, AC005355,	AC012384, AC005288, AL021546, AC006254, AC007536, AC005031, AL035420, AL022165,	AC004655, AC004583, AC004876, AC005529, AP000044, AL049776, AF003626, AF196971,	Z68284, AC007314, AC006130, AL034420, AP000112, AP000504, AC002299, U62292,	AL109984, AC006285, AC005952, Z84466, AC006141, AL049569, AC004675, AL009181,	AC005237, AC005730, AC005772, AL031282, Z83826, AP000558, AC007384, AL031587,	AC007387, AL050341, AL135744, AC008372, AC006011, AC005618, AP000113, AC000026,	AF196970, AC002094, AC006014, AC007226, AC002395, U63630, AF001549, AP000692,	AC006441, AC004859, Z97056, AL080243, U91321, AC005632, AF006501, AC006101,	AF134726, AC005212, AC002316, AC004755, AD001527, AL109827, AC005756, Z95116,	AC006941, AL022324, AC006449, AP000248, D8/6/3, AF038438, AC004941, AL02099/,
15 - 463	15 - 363	15-456	15 - 420	15 - 420				·																												
1 - 449	1 - 349	1 - 442	1 - 406	1 - 406																																
913675	881486	751410	579033	960058																				,												
587	885	589	590	165																																
HCUEP01	HCUEQ37	HCUEQ56	HCUES29	HCUES34																															1.	

HCUERTS 594 576408 1 - 145 15 - 12-20 AC00250, AC007250, AC005270, AC005270, AC005281,							AFONOTA FOREACT A COLICIA 1 5230000 A 107101 A 107101 A 107101 A 107101 A
HCUENTIS 593 657258 1-415 15-429 HCUETTIS 593 657258 1-160 15-174 HCUETTIS 594 506339 1-167 15-181 HCUEULO 595 964857 1-269 15-283 HCUEULO 596 970780 1-274 15-288 HCUEVIT 598 905316 1-1428 15-1442 HCUEVIT 598 905316 1-1428 15-1442							AC002303, AL033000, AC003761, AF003333, AL121003, AL021707, AC007283, AC000344, AL133243, AC007263, AC005277, and AC007229.
HCUET13 593 657258 1 - 160 15 - 174 HCUET27 594 506339 1 - 167 15 - 181 HCUEU10 595 964857 1 - 269 15 - 283 HCUEU20 596 970780 1 - 274 15 - 288 HCUEV08 597 959670 1 - 340 15 - 354 HCUEV17 598 905316 1 - 1428 15 - 1442		HCUES93	592	576498	1-415	15 - 429	AC004821.
HCUEVIO 594 506339 1 - 167 15 - 181 HCUEVIO 595 964857 1 - 269 15 - 283 HCUEVOR 597 959670 1 - 274 15 - 288 HCUEVIT 598 905316 1 - 1428 15 - 1442 HCUEVIT 698 905316 1 - 1428 15 - 1442	1	HCUET13	593	657258	1 - 160	15 - 174	AW292137, AL039500, AI248007, AI078021, AI759999, AI476735, and 295437.
HCUEU10 595 964857 1-269 15-283 HCUEU20 596 970780 1-274 15-288 HCUEV08 597 959670 1-340 15-354 HCUEV17 598 905316 1-1428 15-1442		HCUET27	594	506339	1 - 167	15 - 181	AA353854, AC004659, AC004771, AC005914, AC005245, and AC007182.
HCUEV08 597 959670 1-274 15-288 HCUEV08 597 959670 1-340 15-354 HCUEV17 598 905316 1-1428 15-1442		HCUEU10	595	964857	1 - 269	15 - 283	AC007281.
HCUEV17 598 905316 1 - 1428 15 - 1442 HCUEV17 698 905316 1 - 1428 15 - 1442		HCUEU20	969	08/0/6	1 - 274	15 - 288	
HCUEV17 598 905316 1-1428 15-1442		HCUEV08	597	029656	1 - 340	15 - 354	295116.
		HCUEV17	865	905316	1 - 1428	15 - 1442	AA585439, Z28355, Z30131, AI525556, AI535639, AA585101, AI541374, AA585453, AI557731,
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				,			AL041133, AL047183, AL040322, AL041131, AL046330, AL041051, AL041292, AL040119,
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AL043814, AL043848, AL041459, AL041577, AL044201, AL044258, AL046850, T23985, AL03853, AL03853, AL037727, AI526194, AL046994, AL040076, AL040576, AL040576, AL046753, AL045753, AL046994, AL049018, AL040044, AL040576, AL040076, AL039744, R28735, AL045774, AL049078, AL040044, AL040069, AL040075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400075, AL0400077, AL0400077, AL0400075, AL0400075, AL0400075, AL0400075, AL0400007, AL0400075, AL0400007, AL04000007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL0400007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, AL040000007, AL040000007, AL040000007, AL04000007, AL040000007, AL040000007, AL040000007, AL040000007, AL040000007, AL040000007, AL040000007, AL040000007, AL04000007, AL04000007, AL040000007, AL040000007, AL04000007, AL040000007, AL040000007, AL040000007, AL04000007, AL040000007, AL04000007, AL04000007, AL04000007, AL04000007, AL04000007, A							AL043537, Al541523, AL039338, AL042135, AL044064, AL038983, AL039316, AL043923,
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AL041347, Al541535, AL038761, T23957, AL080031, T41289, AL045989, Al556967, Al546828, AA585476, R29177, AL044529, Al525316, Al557787, Al526073, D51250, AL046147, T23888, D80219, Al546891, Al546855, AL039643, Al541508, C16305, Al525320, AL042096, Al526140, D59787, AL037436, AA585434, Al541510, D80043, AL039360, AL037435, C16300, AL039924, D80227, AL045794, Al535983, AL044125, AA585356, AA174170, D57491, AL079852, Al541307, D80240, Al535660, Al557799, Al546875, AA585440, Al541017, AL043441, AL039150, Al541205, AL038821, AL039085, D80134, AL043445, Al541534, Al541534, Al541509, AL039156, D51423, D55233, Al557238, T24112, T24119, AL039564, AL039558, T11051, AL039108, AL039074, AL038837, AL039625,							AL041168, AL049069, AL043444, AL040075, AI557262, AI541514, AL041246, AL040472,
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